

FIGURE 7K

SEQ ID NO:	Genotype
155-160	I/1a
161-176	II/1b
177-180	III/2a
181-185	IV/2b
186	2c
187-190	(V)/3a
191	4a
193	4b
195	4c
197	4d
194	4e
192	4f
198-205	5a
206	6a

SEQ ID NO:	Genotype	100	110	120	130	140	150	160	170	180	190
155-160	I/1a	LLSPGSRPSWGPDP	RR	L-K	L-GF	I-L-A-L-A-R	VL	V-Y	L-S	L-L	LTV-ASA
161-176	II/1b	RR	L-K	L-GF	I-L-a-L-a-R	VL	V-Y	L-S	L-L	L-L	LTI-asa
177-180	III/2a	HR	V-K	L-Gf	i-V-a-L-V-R	VL	V-Y	L-S	L-L	L-L	LII-vsa
181-185	IV/2b	HR	L-k	L-GF	i-V-A-V-V-R	VL	I-Y	L-S	L-L	L-L	LTV-VSA
186	2c	HK	L-K	L-GF	i-V-A-V-V-R	VL	I-Y	L-S	L-L	L-L	LTV-VSA
187-190	(V)/3a	RR	L-K	L-GF	I-L-A-V-V-R	AL	I-F	L-S	L-L	F-L	LII-AAS
191	4a	RR	L-K	L-GF	I-L-A-V-V-R	AV	I-Y	L-S	L-L	L-L	LTV-ASA
193	4b	RR	L-K	L-GF	I-L-A-V-V-R	AV	I-Y	L-S	L-L	L-L	LTV-ASA
195	4c	RR	L-K	L-GF	I-L-A-V-V-R	AV	I-Y	L-S	L-L	L-L	LTV-tsa
197	4d	RR	L-K	L-GF	I-V-A-V-V-R	LL	V-Y	L-S	L-L	L-L	LTV-ASA
194	4e	RR	L-K	L-GF	I-L-A-V-V-R	AL	I-Y	L-S	L-L	F-L	LTI-ASA
192	4f	RR	L-K	L-GF	I-L-A-V-V-R	AV	I-Y	L-S	L-L	L-L	LTV-ASA
198-205	5a	RK	L-K	L-GF	I-L-G-V-V-R	VL	V-Y	L-S	L-L	L-L	LTV-asa
206	6a	RR	L-K	L-GF	I-V-A-L-V-A	AL	I-Y	L-S	L-L	L-L	LTI-ASA

NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF
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C GENE

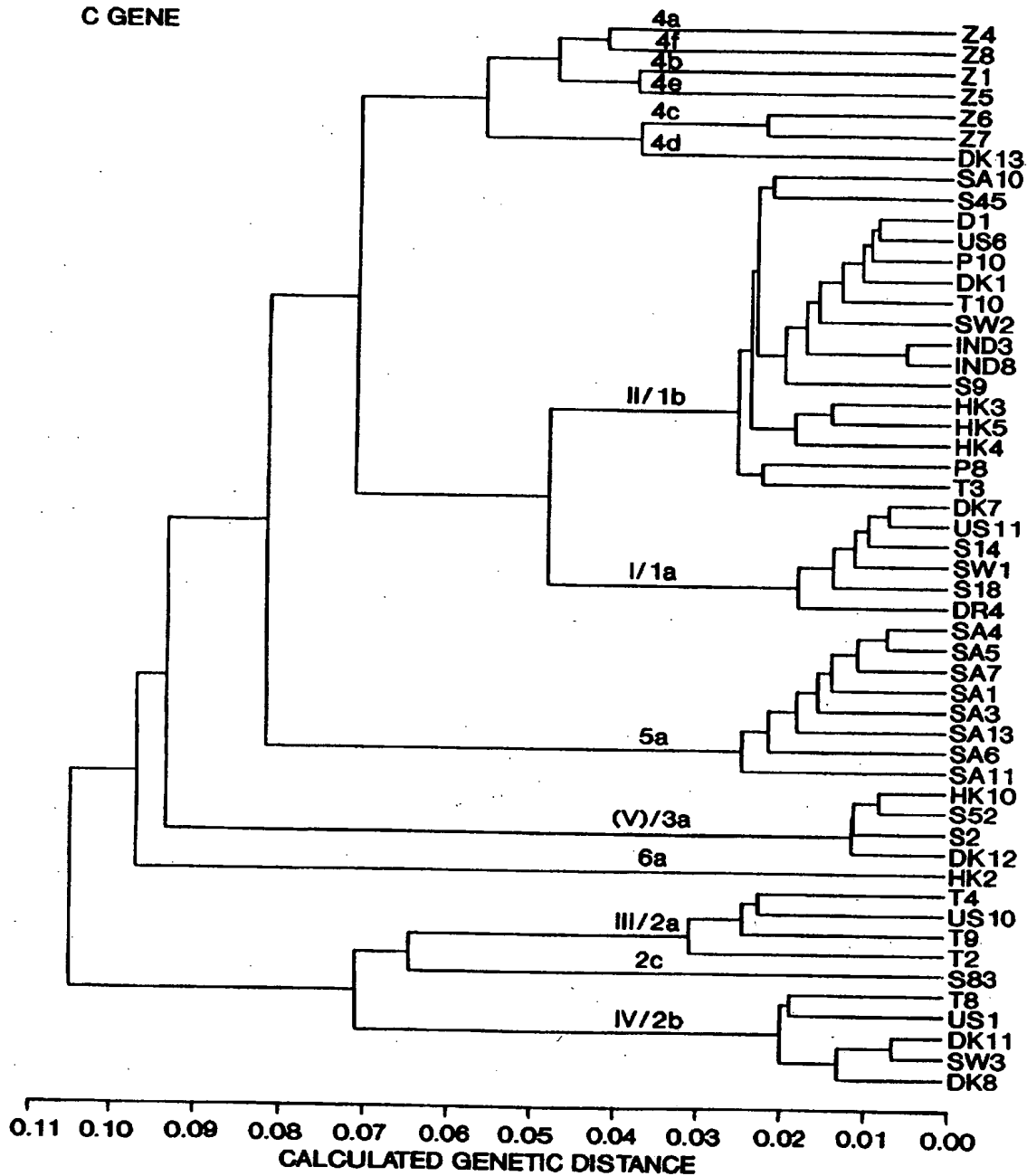


FIG. 8A

NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF
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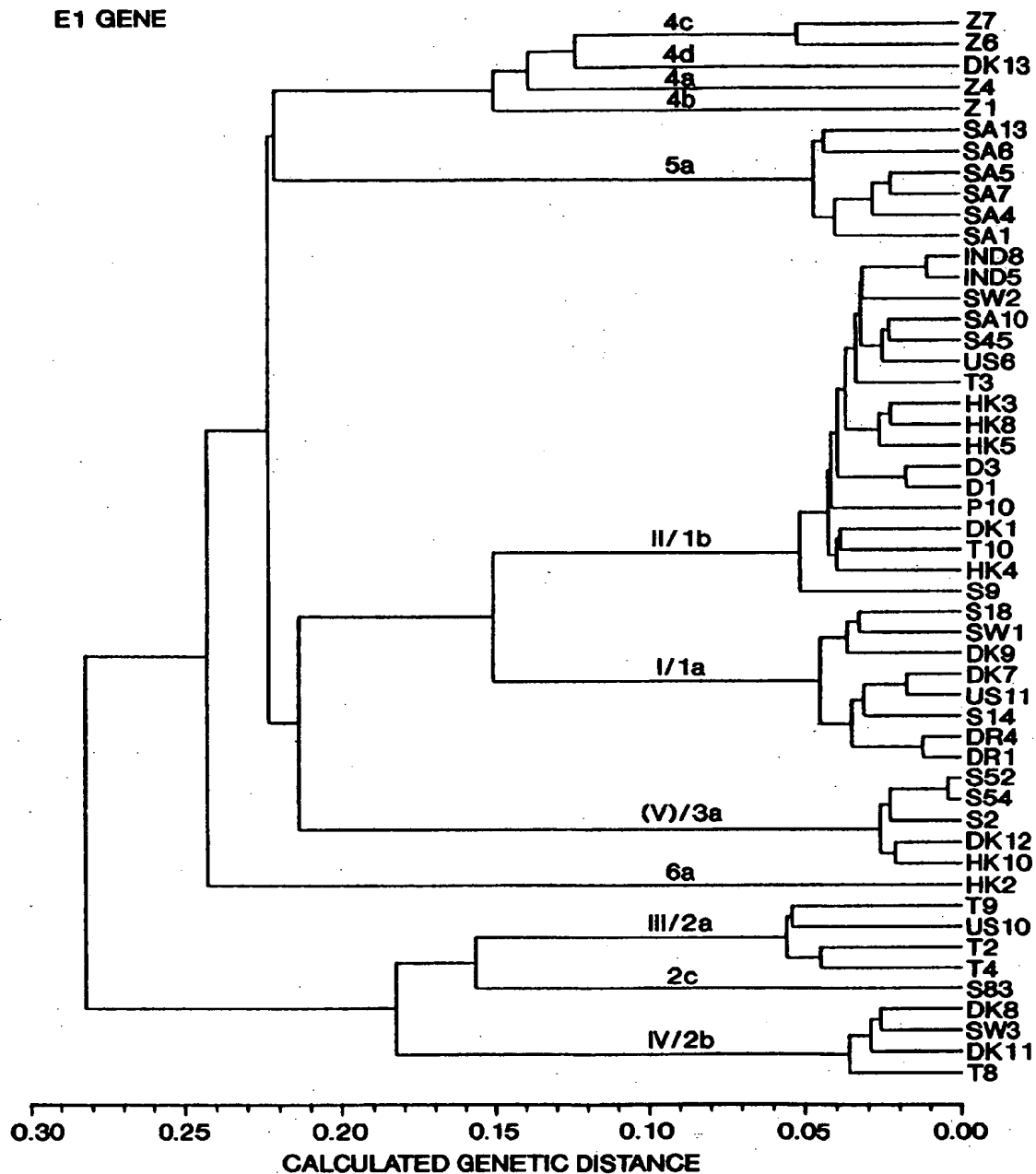


FIG. 8B



SEQ ID NO:	Isolate
5	S14
1	DK7
8	US11
4	DR4
3	DR1
2	DK9
6	S18
7	SW1
1-8	consensus
SEQ ID NO:	Isolate
5	S14
1	DK7
8	US11
4	DR4
3	DR1
2	DK9
6	S18
7	SW1
1-8	consensus

FIGURE 1A-2

SEQ ID NO:	Isolate	
5	S14	123 GGGTAACacCTCGAGGTGTTGGGTGGCGATGACCCCCACGGTGGCCACCAGGGACGGCAAA
1	DK7	123 GGGTAACGtCTCGAGGTGTTGGGTGGCGATGACCCCCACGGTGGCCACCAGGGATGGCAAA
8	US11	123 GGGTAACGctTCGAGGTGTTGGGTGGCGATGACCCCCACGGTGGCCACCAGGGACGGCAAA
4	DR4	123 GGGTAACaCTTCGAGGTGTTGGGTGGCGGTGACCCCCACGGTGGCCACCAGGGACGGCAAA
3	DR1	123 GGGTAACGCCTTCGAGGTGTTGGGTGGCGGTGACCCCCACGGTGGCCACCAGGGACGGCAAA
2	DK9	123 GGGTAACGCCTTCGAaATGTTGGGTGGCGGTGGCCCCACGGTGGCCACCAGGGACGGCAAg
6	S18	123 GGGTAACGCCTTCGagATGTTGGGTGcCGGTGGCCCCCAGTtGCCACCAGGGACGGCAAA
7	SW1	23 GgAtggCGCCcCGAagTgTTGGGTgGCGGTGGCCCCCAGTcGCCAcTAgGGACGGCAAA
1-8	consensus	GGgTaaGgcctCGAggtGTTGGGTGgCGgTgaCCCCCAGcGTgGCCAcCAGGGACGGCAAA
SEQ ID NO:	Isolate	
5	S14	184 CTCCCCgCaaCGCAGCTTCGACGtTACATCGATCTGCTtGTCTGGGAGcGCCACCCCTCTGTT
1	DK7	184 CTCCCCACagCGCAGCTTCGACCTTCACTCGATCTGCTcGTCTGGGAGtGCCACCCCTCTGTT
8	US11	184 CTCCCCAaACGCAaCTTCGACGTCACTCGATCTGCTTGTCTGGGAGCGCCACCCCTCTGTT
4	DR4	184 CTCCCCACAACGCAGCTcCGACGTCACTCGACCTGTGTCTGGGAGCGCCACCCCTCTGCT
3	DR1	184 CTCCCCACAACGCAGCTTCGACGTCACTCGACCTGTGTCTGGGAGCGCCACCCCTCTGCT
2	DK9	184 CTCCCCGCAACGCAGCTTCGACGTCACTCGATCTGCTTGTCTGGGAGCGCCACCCCTCTGCT
6	S18	184 CTCCCCGCAACGCAGCTTCGACGTCACTCGATCTGCTTGTtGGGAGCGCCACCCCTCTGCT
7	SW1	184 CTCCctGCAACGCAGCTTCGACGTCACTCGATCTGCTTGTcGgaAGCGCCACCCCTCTGCT
1-8	consensus	CTCCCCc-CAAcCGCAGCTtCGACGTcACATCGATCTGCTtGTcGGgAGcGCCACCCCTCTGcT

NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF
THE ENVELOPE 1...

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FIGURE 1A-3

SEQ ID NO:	Isolate	
5	S14	245 CGGCCCTCTACGTGGGGGACCTGTGCGGGTCTGTCTTTCTTGTGGTCAGCTGTTTACCTT
1	DK7	245 CGGCCCTCTACGTGGGGGACCTGTGCGGGTCTGTCTTTCTTGTGGTCAGCTGTTTACCTT
8	S11	245 CGGCCCTCTACGTGGGGGACCTGTGCGGGTCTGTCTTTCTTGTGGTCAGCTGTTTACCTT
4	DR4	245 CGGCCCTCTACGTGGGGGACCTGTGCGGGTCTGTCTTTCTTGTGGTCAGCTGTTTACCTT
3	DR1	245 CGGCCCTCTACGTGGGGGACCTGTGCGGGTCTGTCTTTCTTGTGGTCAGCTGTTTACCTT
2	DK9	245 CGGCCCTCTATGTGGGGGACCTGTGCGGGTCTGTCTTTCTTGTGGTCAGCTGTTTACCTT
6	S18	245 CGGCCCTCTATGTGGGGGACCTGTGCGGGTCTGTCTTTCTTGTGGTCAGCTGTTTACCTT
7	SW1	245 CGGCCCTCTACGTGGGGGACCTGTGCGGGTCTGTCTTTCTTGTGGTCAGCTGTTTACCTT
1-8	consensus	CGGCCCTCTACGTGGGGGAC - TGTGCGGGTCTGTCTTTCTTGTGGTCAGCTGTTTACCTT
5	S14	306 CTCTCCAGGCGCCCTCTGGACGACGCAAGACTGCAATTGTTCTATCTATCCCGGCCATATA
1	DK7	306 CTCTCCAGGCGCCCTCTGGACGACGCAAGGCTGCAATTGTTCTATCTATCCCGGCCATATA
8	S11	306 CTCTCCAGGCGCCCTCTGGACGACGCAAGGCTGCAATTGTTCTATCTATCCCGGCCATATA
4	DR4	306 CTCTCCAGGCGCCCTCTGGACGACGCAAGGCTGCAATTGTTCTATCTATCCCGGCCATATA
3	DR1	306 tTCTCCAGGCGCCCTCTGGACGACGCAAGGCTGCAATTGTTCTATCTATCCCGGCCATATA
2	DK9	306 CTCTCCAGGCGCCCTCTGGACGACGCAAGGCTGCAATTGTTCTATCTATCCCGGCCATATA
6	S18	306 CTCTCCAGGCGCCCTCTGGACGACGCAAGGCTGCAATTGTTCTATCTATCCCGGCCATATA
7	SW1	306 CTCTCCAGGCGCCCTCTGGACGACGCAAGGCTGCAATTGTTCTATCTATCCCGGCCATATA
1-8	consensus	cTctCCcAGgCgCCaCTGGACaACGCAaGaCTGcAAtTgTtTctATctATcCCcGGCCATaTa

NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF
THE ENVELOPE 1...

Bukh et al.

Appl. No.: 09/084,691 Atty Docket: NIH240.1CPDV1
REPLACEMENT SHEET

FIGURE 1A-4

SEQ ID NO:	Isolate	
5	S14	367 ACGGTCATCGCATGGCaTGGGATATGATGAACCTGGTCCCCTACgACGGcAcTGGTAG
1	DK7	367 ACGGTCACCGCATGGCGTGGGATATGATGAACCTGGTCCCCTACcACGGCGTTGGTAG
8	S11	367 ACGGTCACCGCATGGCaTGGGATATGATGAACCTGGTCCCCTACgCGGCGTTGGTgG
4	DR4	367 ACGGcCACCGCATGGCGTGGGATATGATGAACCTGGTCCCCTACgACAGCGCTGGTAG
3	DR1	367 ACGGgACACCGtATGGCaTGGGATATGATGAACCTGGTCCCCTACgACAGCGCTGGTAA
2	DK9	367 ACGGTCATCGcATGGCGTGGGATATGATGAACCTGGTCCCCTACAGCAGCGCTGGTAA
6	S18	367 ACGGTCACCGtATGGCATGGGATATGATGAACCTGGTCCCCTACAAcGCGgtTGGTAA
7	SW1	367 ACGGTCACCGcATGGCATGGGATATGATGAACCTGGTCCCCTACAAcAGCGcTGGTAG
1-8	consensus	ACGGtCacCGcATGGCaTGGGATATGATGAACCTGGTCCCCTACgAc-GCgcTGGTag
5	S14	428 TAGCTCAGCTGCTCCGGATCCCaCAAGCCATCTTGGATATGATCGCTGGTGTCTCACTGGGG
1	DK7	428 TAGCTCAGCTGCTCCGGATCCCGCAAGCCATCTTGGACATGATCGCTGGTGTCTCACTGGGG
8	S11	428 TAGCTCAGCTGCTCCGGATCCCaCAAGCCATCTTGGACATGATCGCTGGTGTCTCACTGGGG
4	DR4	428 TAGCTCAGCTGCTCCGGATCCCaCAAGCCATCTTGGACATGATCGCTGGTGTCTCACTGGGG
3	DR1	428 TGGCTCAGCTGCTCCGGATCCCaCAAGCCATCTTGGACATGATCGCTGGTGTCTCACTGGGG
2	DK9	428 TGGCGCAGCTGCTCAGGATCCCGcAGGCCATCTTGGACATGATCGCTGGTGTCTCACTGGGG
6	S18	428 TAGCTCAGCTGCTCAGGgTCCCGCAAGCCGTCTTGGACATGATCGCTGGTGTCTCACTGGGG
7	SW1	428 TAGCTCAGCTGCTCAGGaTCCCGCAAGCCGTCTTGGACATGATCGCTGGTGTCTCACTGGGG
1-8	consensus	TagCTCAGCTGCTCcGGaTCCC-CAAGCCaTCTTGGAcATGATCGCTGGTGTCCcCACTGGGG

FIGURE 1A-5

SEQ ID NO:	Isolate	
5	S14	489 AGTCCTAGCGGGCATAGCGTATTCTCCATGTTGGGAACCTGGCGAAGGTCCCTaGTgGTG
1	DK7	489 AGTCCTgCGGGCATAGCGTATTCTCCATGTTGGGAACCTGGCGAAGGTCCCTGTTAGTG
8	S11	489 AGTCCTAGCGGGCATAGCGTATTCTCCATGTTGGGAACCTGGCGAAGGTCCCTGTTAGTG
4	DR4	489 AGTCCTAGCGGGCATAGCGTATTCTCCATGTTGGGAACCTGGCGAAGGTCCCTGTTAGTG
3	DR1	489 AGTCCTAGCGGGCATAGCGTATTCTCCATGTTGGGAACCTGGCGAAGGTCCCTGTTAGTG
2	DK9	489 AGTCCTAGCGGGCATAGCGTATTCTCCATGTTGGGAACCTGGCGAAGGTCCCTGTTAGTG
6	S18	489 AGTCCTAGCGGGCATAGCGTATTCTCCATGTTGGGAACCTGGCGAAGGTCCCTGTTAGTG
7	SW1	489 AGTCCTAGCGGGCATAGCGTATTCTCCATGTTGGGAACCTGGCGAAGGTCCCTGTTAGTG
1-8	consensus	AGTCCTAGCGGGCATAGCGTATTCTCCATGTTGGGAACCTGGCGAAGGTCCCTgGTgGTg

SEQ ID NO:	Isolate	
5	S14	550 CTGCTGCTATTGCCCGCGTtGACGCG
1	DK7	550 CTGCTGCTATTGCCCGCGTcGACGCG
8	US11	550 CTGCTGCTATTGCCCGCGTcGACGCG
4	DR4	550 CTGTTGCTGTTGCCCGCGTtGATGCG
3	DR1	550 CTGTTGCTGTTGCCCGCGTtGATGCG
2	DK9	550 CTGTTGCTGTTaCCGCGCTCGATGCG
6	S18	550 CTGTTGCTGTTgCCGCGCTCGATGCG
7	SW1	550 CTGTTGCTGTTtCCGCGCTCGATGCG
1-8	consensus	CTGtTGCTgTtTtgCCGCGCGTcGAtGCG

FIGURE 1B-1

SEQ ID NO:	Isolate	
11	DK1	1 TATGAAGTGGCAACGTGTCCGGGGTGTACCACTGTCaAACGACTGCTCCAACCTCAAGCA
24	T10	1 TATGAAGTGGCAACGTGTCCGGGGTGTACCACTGTCaAACGACTGCTCCAACCTCAAGCA
10	D3	1 TATGAAGTGGCAACGTGTCCGGGGTGTACCACTGTCaAACGACTGCTCCAACCTCAAGCA
9	D1	1 TATGAAGTGGCAACGTGTCCGGGGTGTACCACTGTCaAACGACTGCTCCAACCTCAAGCA
14	HK5	1 TATGAAGTGGCAACGTGTCCGGGGTGTACCACTGTCaAACGACTGCTCCAACCTCAAGCA
15	HK8	1 TATGAAGTGGCAACGTGTCCGGGGTGTACCACTGTCaAACGACTGCTCCAACCTCAAGCA
12	HK3	1 TATGAAGTGGCAACGTGTCCGGGGTGTACCACTGTCaAACGACTGCTCCAACCTCAAGCA
23	T3	1 TACGAAGTGGCAACGTGTCCGGGGTGTACCTATGTCaACGAACTGCTCCAACCTCAAGCA
22	SW2	1 TATGAAGTGGCAACGTGTCCGGGGTGTACCTATGTCaACGAACTGCTCCAACCTCAAGCA
17	IND8	1 TATGAAGTGGCAACGTGTCCGGGGTGTACCTATGTCaACGAACTGCTCCAACCTCAAGTA
16	IND5	1 TATGAAGTGGCAACGTGTCCGGGGTGTACCTATGTCaACGAACTGCTCCAACCTCAAGTA
21	SA10	1 TATGAAGTGGCAACGTGTCCGGGGTGTACCTATGTCaACGAACTGCTCCAACCTCAAGCA
20	S45	1 TATGAAGTGGCAACGTGTCCGGGGTGTACCTATGTCaACGAACTGCTCCAACCTCAAGCA
25	US6	1 TATGAAGTGGCAACGTGTCCGGGGTGTACCTATGTCaACGAACTGCTCCAACCTCAAGCA
13	HK4	1 cATGAAGTGGCAACGTGTCCGGGGTGTACCTATGTCaACGAACTGCTCCAACCTCAAGTA
18	P10	1 TATGAAGTGGCAACGTGTCCGGGGTGTACCTATGTCaACGAACTGCTCCAACCTCAAGTA
19	S9	1 TATGAAGTGGCAACGTGTCCGGGGTGTACCTATGTCaACGAACTGCTCCAACCTCAAGTA
9-25	consensus	tAtGaaGTGcgCAACGTGTCCGGGGTGTaccAtGTcACgAAcGACTGcTCCAACTcaAGca

FIGURE 1B-2

SEQ ID NO:	Isolate	
11	DK1	62 TcGTGTATGAGGCAGTGGACGTGATCATGTCATACCCCaGGGTGGTGCCTGCCTTCGGGA
24	T10	62 TtGTGTATGAGGCAGCGGACCTTGATCATGCACACCCCGGGTGGTGCCTGCCTTCGGGA
10	D3	62 TcGTGTATGAGGCAGCGGACATGATCATGCACACCCCGGGTGGTGCCTGCCTTCGGGA
9	D1	62 TtGTGTATGAGGCAGCGGACATGATCATGCACACCCCGGGTGGTGCCTGCCTTCGGGA
14	HK5	62 TCGTGTACGAGACaACCGGACATGATCATGCACACCCCTGGGTGGTGCCTGCCTTCGGGA
15	HK8	62 TCGTGTATGAAACAGCGGACATGATCATGCATACCCCTGGATGCCTGCCTTCGGGA
12	HK3	62 TCGTGTATGAGACAGACATGATCATGCATACCCCTGGATGCCTGCCTTCGGGA
23	T3	62 TTGTGTATGAGACAGCGGACATGATCATGCACACCCCTGGGTGGTGCCTGCCTTCGGGA
22	SW2	62 TTGTGTATGAGACAGCGGACATGATCATGCATACCCCGGGTGGTGCCTGCCTTCGGGA
17	IND8	62 TTGTGTATGAGGCAGCGGACATGATCATGCACACCCCGGGTGGTGCCTGCCTTCGGGA
16	IND5	62 TTGTGTATGAGGCAGCGGACATGATCATGCACACTCCCGGGTGGTGCCTGCCTTCGGGA
21	SA10	62 TTGTGTATGAGGCAGCGGACATGATCATGCACACCCCGGGTGGTGCCTGCCTTCGGGA
20	S45	62 TTGTGTATGAGGCAGTGGACGTGATCCTGCACACCCCTGGGTGGTGCCTGCCTTCGGGA
25	US6	62 TTGTGTATGAGGCAGCGGACATGATCATGCACACTCCCGGGTGGTGCCTGCCTTCGGGA
13	HK4	62 TTGTGTATGAGGCAGCGGACATGATCATGCATACCCCGGGTGGTGCCTGCCTTCGGGA
18	P10	62 TTGTGTATGAGGCAGCGGACATGATCATGCACACCCCGGGTGGTGCCTGCCTTCGGGA
19	S9	62 TTGTGTACGAGGCAGCGGACGTGATCATGTCATACCCCGGGTGGTGCCTGCCTTCGGGA
9-25	consensus	TtGTGTATGAGGCAGCGGACATGATCaTGCaACCCCGGGGTGGcTgCCCCTGCcGTTcCGGA

FIGURE 1B-3

SEQ ID NO:	Isolate	
11	DK1	123 GaaCAACcaCTCCCGtTGCTGGGTAGCGCTCAcCCcACGCTCGCGGCCAGGAACgCCAGC
24	T10	123 GgCAACTCCTCCCGTGTGGGTAGCGTCACTCCcACGCTCGCGGCCAGGAACcACCAGC
10	D3	123 GGACAACTCCTCTCGCTGTGGGTAGCGCTCAcCCcACGCTCGCGGCCAGGAATAGCAGC
9	D1	123 GGACAACTCCTCTCGCTGTGGGTAGCGCTCAcCCcACGCTCGCGGCCAGGAATGGCAaC
14	HK5	123 aAACAACTCCTCCCGTGTGGGTAGCGCTGcCCCCACGCTCGCGGCCAGGAACGcCAGC
15	HK8	123 GAACAACTCCTCCCGTGTGGGTAGCGCTCACTCCcACGCTCGCGGCCAGGAATGTcAGC
12	HK3	123 GAACAACTCCTCCCGTGTGGGTAGCGCTCACTCCcACGCTCGCGGCCAGGAACGTcAGC
23	T3	123 GAgCAATTCCTCCCGTGTGGGTAGCGCTtACTCCcACGCTCGCGGCCAGGAACGCCAGC
22	SW2	123 GgCAACTCCTCCCGTGTGGGTAGCGCTCACTCCcACGCTAGCaGCCAGGAACaCCAGC
17	IND8	123 GGGCAACTtCTCTAgTtTGCTGGGTAGCGCTCACTCCcACTCTCGCGGCCAGGAACGcCAGC
16	IND5	123 GGGCAACTCCTCTCGCTGTGGGTAGCGCTCACTCCcACTCTCGCGGCCAGGAACGCCAGC
21	SA10	123 GAACAACTCCTCCCGTGTGGGTAGCGCTCACTCCcACGCTCGCGGCCAGGAACCTCCAGC
20	S45	123 GAACAACTCCTCCCGtTGCTGGGTgCGGTCACTCCcACGCTCGCGGCCAGGAACCTCCAGC
25	US6	123 GAACAACTCCTCCCGtTGCTGGGTAGCGTCACTCCcACGCTCGCGGCCAGGAACGTtAGC
13	HK4	123 GAACAACTCCTCCCGtTGCTGGGTAGCGTCACTCCcACGCTCGCGGCCAGGAACGCCAGC
18	P10	123 GAACAACTCCTCCCGtTGCTGGGTAGCGTCACTCCcACaCTCGCGGCCAGGAATtCCAGC
19	S9	123 GggtAACTCTCTCCCAaTGCTGGGTgCGGTCAcCCcCAcGCTCGCGGCCAGGAACgTtAcc
9-25	consensus	gaacAActcCTCccgcTGcTGGGTaGGCTCaCtCCCACgCTcGCgGCCAGGAACgcccAgC

FIGURE 1B-4

SEQ. ID NO:	Isolate	
11	DK1	184 aTCCCCACTACGACaATACGACGCCATGTCGATTGCTCGTTGGGGCGGCTGCTTTCTGCT
24	T10	184 GTCCCCACTACGACgATACGACGCCATGTCGATTGCTCGTTGGGGCGGCTGCTTTCTGCT
10	D3	184 GTCCCCACTACGACaATACGACGCCACGTTCGATTGCTCGTTGGGGCGGCTGCTTTCTGCT
9	D1	184 GTCCCCACTACGGCgATACGACGCCACGTTCGATTGCTCGTTGGGGCGGCTGCTTTCTGCT
14	HK5	184 GTCCCCACaACGGCAATACGACGCCACGTTCGATTGCTCGTTGGGGCGGCTGCTTTCTGCT
15	HK8	184 GTCCCCACTACGACaATACGACGCCACGTTCGATTGCTCGTTGGGGCGGCTGCTTTCTGCT
12	HK3	184 GTCCCCACaACGACAATACGACGTTCGATTGCTCGTTGGGGCGGCTGCTTTCTGCT
23	T3	184 GTCCCCACTAaGACAATACGACGTTCGATTGCTCGTTGGGGCGGCTGCTTTCTGCT
22	SW2	184 GTCCCCACTACGACaATACGACGCCACGTTCGATTGCTCGTTGGGGCGGCTGCTTTCTGCT
17	IND8	184 GTCCCCACACGACAATACGACGCCACGTTCGATTGCTCGTTGGGGCGGCTGCTTTCTGCT
16	IND5	184 GTcTCCACACGACAATACGACaCCACGTTCGATTGCTCGTTGGGGCGGCTGCTTTCTGCT
21	SA10	184 GTCCCCACTACGACAATACGACGCCACGTTCGATTGCTCGTTGGGGCGGCTGCTTTCTGCT
20	S45	184 GTCCCCACTACGACAATACGACGTTCGATTGCTCGTTGGGGCGGCTGCTTTCTGCT
25	US6	184 GTCCCCACTACGACAATACGACGCCACGTTCGATTGCTCGTTGGGGCGGCTaCTTTCTGCT
13	HK4	184 aTCCCCACTACGACAATACGACGCCATGTCGATTGCTCGTTGGGGCGGCTGCTTTCTGCT
18	P10	184 GTCCCCACTACGgCAATACGACGCCATGTCGATTGCTCGTTGGGGCGGCTGCTTTCTGCT
19	S9	184 GTCCCCaACcAGGaCAATACGACGTCAATGTCGATTGCTCGTTGGGGCGGCTGCTTTCTGCT
9-25	consensus	gTCCcCcAcTAcGaCaATACGACgCaCGTCGATTTGCTCGTTGGGGCGGCTgctTTCTGCT

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FIGURE 1B-5

SEQ ID NO.	Isolate	
11	DK1	245 CCGCTATGTACGTGGGGGACCTCTGCGGATCCGTTTCTCGTCTCTCAGCTGTTCAACCTT
24	T10	245 CCGCTATGTATGTGGGAGACCTCTGCGGATCTGTTTCTCGTCTCTCAGCTGTTCAACCTT
10	D3	245 CCGCCATGTACGTGGGGGATCTTGGCGGATCTGTTTCTCGTCTCCAGCTGTTCAACCTT
9	D1	245 CCGCCATGTACGTGGGGGATCTTGGCGGATCTGTTTCTCTCaTCTCCAGCTGTTCAACCTT
14	HK5	245 CCGCTATGTACGTGGGGGATCTTGGCGGATCTGTTTCTCGTCTCCAGCTGTTCAACCTT
15	HK8	245 CCGCTATGTACGTGGGGGATCTCTGCGGATCTGTTTCTCGTCTCCAGCTGTTCAACCTT
12	HK3	245 CCGCTATGTACGTGGGGGATCTCTGCGGATCTGTTTCTCGTCTCCAGCTGTTCAACCTT
23	T3	245 CCGCTATGTACGTGGGGGATCTCTGCGGATCTGTTTCTCGTCTCCAGCTGTTCAACCTT
22	SW2	245 CCGtTATGTACGTGGGGGATCTCTGCGGATCTGTTTCTCGTCTCCAGCTGTTCAACCTT
17	IND8	245 CCGCTATGTACGTGGGGGATCTCTGCGGATCTGTTTCTCGTCTCCAGCTGTTCAACCTT
16	IND5	245 CCGCTATGTACGTGGGGGATCTaTGGCGGATCTGTTTCTCGTCTCCAGCTGTTCAACCTT
21	SA10	245 CCGCcatGTACGTGGGGGACCTCTGCGGATCTGTTTCTCGTCTCCAGCTGTTCAACCTT
20	S45	245 CCGCTATGTACGTGGGGGATCTCTGCGGATCTGTTTCTCGTCTCCAGCTGTTCAACCTT
25	US6	245 CCGCTATGTACGTGGGGGACCTCTGCGGGTCcGTTTCTCTCaTCTCCAGCTGTTCAACCTT
13	HK4	245 CCGCcatGTACGTGGGAGATCTCTGCGGATCTGTCTCTCGTCTCCAGTGTGTTCAACCTT
18	P10	245 CCGCTATGTACGTGGGGGATCTCTGCGGATCTGTTCTCTCGTCTCCAGCTGTTCAACCTT
19	S9	245 CCGCTATGTACGTGGGGGACtGtGCGGATCTGTTTTCCTCaTCTCCAGCTGTTCAACCaT
9-25	consensus	CCGctATGTACGTGGGGGATCTcTGGGGaTCTcGTtTtTCCTcgTcTcCaAGcTGTTCACcctT

NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF
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FIGURE 1B-6

SEQ ID NO:	Isolate	
11	DK1	306 tTCaCTCGCCGGCATGAGACagcaCAGGACTGCAACTGCTCAATCTATCCCGGCCAcgTt
24	T10	306 CTCGCCCTCGCCGGCATGAGAcTtTgCAGGACTGCAACTGCTCAATCTATCCCGGCCAcTtG
10	D3	306 CTCGCCCTCGCCGGCATGAGACaGTACAGGAaTGTAACTGCTCAATCTATCCCGGCCAcGtG
9	D1	306 CTCGCCCTCGCCGGCATGAGACGGTACAGGAGTGTAACTGCTCAATCTATCCCGGCCAcGtG
14	HK5	306 CTCGCCCTCGCCGGCACACGAGACGGTACAGGACTGCAACTGCTCAATCTATCCCGGCCAcGTA
15	HK8	306 tTCGCCCTCGCCGGCACACGAGACGGTACAGGACTGCAACTGCTCAATCTATCCCGGCCAcGTA
12	HK3	306 CTCGCCCTCGCCGGCACACGAGACGGTACAGGACTGCAACTGCTCACTCTATCCCGGCCAcGTA
23	T3	306 CTCGCCCTCGCCGGCAtGAGACAGTACAGGACTGCAACTGCTCAATCTATCCCGGCCAcGTA
22	SW2	306 tTCACCTCGCCGGCACGAGACAGTACAGGACTGCAACTGCTCACTCTATCCCGGCCAcGTA
17	IND8	306 CTCACCGCGCCGGCATGAGACAGTACAGGACTGCAATTGCTCCATCTATCCCGGCCAcGTA
16	IND5	306 CTCACCGCGCCGGCATGAGACAGTACAGGACTGCAATTGCTCCATCTATCCCGGCCAcGTA
21	SA10	306 CTCGCCCTCGCCGGTAtGAGACAGTACAGGACTGCAATTGCTCAATCTATCCCGGCCGcGTA
20	S45	306 CTCGCCCTCGTCGGCATGAGACAGTACAGGACTGCAACTGTTCAATCTATCCCGGCCAcGTA
25	US6	306 CTCGCCCTCGTCaGCATGAGACAGTACAGGACTGCAATTGTTCAATCTATCCCGGCCAcGTA
13	HK4	306 CTCGCCCTCGCCGGCATGAGAcGtTACAGGACTGCAATTGCTCAATCTATCCCGGCCAcGTA
18	P10	306 CTCaCCTCGCCGGCATtGACAGTACAGGACTGCAATTGTTCAATCTATCTCTCGGCCAcGTA
19	S9	306 CTCgCCcCGtCGGCATgaGACAGTACAGaACTGCAATTGCTCAATCTATCTCTCGGgaCAGTg
9-25	consensus	cTCgCCTCGcCggcAtgaGACagtaCAGgAcTGcAAcTGcTcaaTCTATCTCTCGGcCacgTa

FIGURE 1B-7

SEQ ID NO:	Isolate	
11	DK1	367 TCAGGTCACCGCATGGCTTGGGATATGATGAACTGGTcACCTACAACAGCCCTAGTGG
24	T10	367 TCAGGTCACCGCATGGCTTGGGACATGATGAACCTGGTCGCTACAACAGCCTTAGTGG
10	D3	367 ACAGGTCACCGCATGGCTTGGGATATGATGAACTGGTCGCTACAGCAGCCCTAGTGG
9	D1	367 ACAGGTCACCGCATGGCTTGGGATATGATGAACTGGTCACCTACAACAGCCTTAGTGG
14	HK5	367 ACAGGTCACCGCATGGCTTGGGATATGATGAACCTGGTCACCTACAACAGCCCTAGTGG
15	HK8	367 TCAGGTCACCGCATGGCTTGGGATATGATGAACTGGTCGCCAACAGCCCTAGTGG
12	HK3	367 TCAGGTCACCGCATGGCTTGGGATATGATGAACCTGGTCCTACAGCAGCCCTAGTGG
23	T3	367 aCAGGTCACCGtATGGCTTGGGATATGATGAACTGGTCGCCaACaCgGCaCTAGTGG
22	SW2	367 TCAGGTCACCGCATGGCTTGGGACATGATGAACCTGGTCACCTACAGCaGCCCTgTGG
17	IND8	367 TCAGGTCACCGCATGGCTTGGGATATGATGAACTGGTCACCTACAGCgGCCCTAGTGG
16	IND5	367 TCAGGTCACCGCATGGCTTGGGATATGATGAACCTGGTCACCTACAGCAGCCCTAGTGG
21	SA10	367 ACAGGTCACCGCATGGCTTGGGATATGATGAACCTGGTCACCTACAaCAGCtCTAGTaG
20	S45	367 ACAGGTCACCGCATGGCTTGGGATATGATGAACCTGGTCCTACAGCAGCctTAGTGG
25	US6	367 TCAGGTCACCGCATGGCTTGGGATATGATGAAT TGGTCACCTACAGCAGCCCTAGTGG
13	HK4	367 TCAGGTCACCGCATGGCTTGGGATATGATGAACCTGGTCACCTACAGCAGCCCTAGTGG
18	P10	367 TCAGGTCACCGCATGGCTTGGGATATGATGAACCTGGTCGCCcACAGCAGCCCTAGTGG
19	S9	367 aCAGGTCatCGCATGGCtTGGGATATGATGAACCTGGTCGCCtACaACAGCCCTAGTGG
9-25	consensus	tCAGGTCaCGcATGGCtTGGGATATGATGAACtGGTcACCTACAGCaGCCcTaGTg

FIGURE 1B-8

SEQ ID NO:	Isolate	
11	DK1	428 TaTCGCAGTTACTCCGgaATCCCACAAGCTGTCTGGACATGGTgGcGgGGGGCCCCACTGGGG
24	T10	428 TgTCGCAGTTACTCCGGATCCCACAAGCTGTCTGGACATGGTgCaCaGGGGCCCCACTGGGG
10	D3	428 TaTCGCAGTTACTCCGGATCCCACAAGCTGTCTGGACATGGTgGcGgGGGGCCCCACTGGGG
9	D1	428 TaTCGCAGTTACTCCGGATCCCACAAGCTGTCTGGACATGGTgGcGgGGGGCCCCACTGGGG
14	HK5	428 TgTCGCAGTTACTCCGGATCCCACAAGCTGTCTGGACATGGTgGcGgGGGGCCCCACTGGGG
15	HK8	428 TgTCGCAGTTACTCCGGATCCCACAAGCTGTCTGGACATGGTgGcGgGGGGCCCCACTGGGG
12	HK3	428 TgTCGCAGTTACTCCGGATCCCACAAGCTGTCTGGACATGGTgGcGgGGGGCCCCACTGGGG
23	T3	428 TgTCGCAGTTgCTCCGGATCCCACAAGCTGTCTGGACATGGTgGcGgGGGGCCCCACTGGGG
22	SW2	428 TaTCGCAGTTaCTCCGGATCCCACAAGCTGTCTGGACATGGTgGcGgGGGGCCCCACTGGGG
17	IND8	428 TaTCGCAGTTGCTCCGGATCCCACAAGCTGTCTGGATATGGTgGcGgGGGGCCCCACTGGGG
16	IND5	428 TaTCGCAGTTGCTCCGGATCCCACAAGCTGTCTGGATATGGTgGcGgGGGGCCCCACTGGGG
21	SA10	428 TaTCGCAGTTACTCCGGATCCCACAAGCTaTCGTGGACATGGTgGcGgGGGGCCCCACTGGGG
20	S45	428 TaTCGCAGTTACTCCGGATCCCACAAGCTGTCTGGACATGGTgGcGgGGGGCCCCACTGGGG
25	US6	428 TaTCGCAGTTACTCCGGATCCCACAAGCTGTCTGGACATGGTgGcGgGGGGCCCCACTGGGG
13	HK4	428 TaTCGCAGTTACTCCGacTCCCACAAGCTGTCTGGACATGGTgGcGgGGGaGCCCCACTGGGG
18	P10	428 TgTCGCAGTTACTCCGGATCCCACAAGTTaTCTGGATgTGGTgGcGgGGGGCCCCACTGGGG
19	S9	428 TaTCGCAGTTACTCCGGATCCCACAAGCTgTCTGGATaTGGTgGcGgGGGGCCCCACTGGGG
9-25	consensus	TaTCGCAGtTaCTCCGgaTCCCACAAGCTgTCGTGGAcCaTGGTgGcGgGGGGCCCCACTGGGG

FIGURE 1B-9

SEQ ID NO:	Isolate	
11	DK1	489 AGTCCTGGCGGCTcGCCTACTACTCCATGGCGGGAACTGGGCCaAGGTTTAAATTGTG
24	T10	489 AGTCCTGGCGGCTcGCCTACTACTCCATGGCGGGAACTGGGCTAAGGTTTAAATTGTG
10	D3	489 GGTCTGGCGGCTCGCCTACTATTCCATGTGGGAACTGGCTAAGGTTTGAATTGTG
9	D1	489 GGTCTGGCGGCTCGCCTACTATTCCATGTGGGAACTGGGCTAAGGTTTGAATTGTG
14	HK5	489 GGTCTGGCGGCTCGCCTACTATTCCATGTGGGAACTGGGCTAAGGTTTGAATTGTG
15	HK8	489 AGTCCTAGCGGCTTGCCCTACTATTCCATGTGGGcAACTGGGCTAAGGTTTGAATTGTG
12	HK3	489 AGTCCTAGCGGCTTGCCCTACTATTCCATGTGGGAACTGGGCTAAGGTTTGAATTGTG
23	T3	489 AGTCCTGGCGGCTTGCCCTACTATTCCATGTGGGAACTGGGCTAAGGTTTGAATTGTG
22	SW2	489 AGTCCTGGCGGCTTGCaTACTATTCCATGTGGGAACTGGGCTAAGGTTTGAATTGTG
17	IND8	489 AATCCTGGCGGCTTGCCCTACTATTCCATGTAGGAACTGGGCTAAGGTTTGAATTGTG
16	IND5	489 AATCCTGGCGGCTTGCCCTACTATTCCATGTAGGAACTGGGCTAAGGTTTGAATTGTG
21	SA10	489 AGTCCTaGCGGCTTGCCCTACTATTCCATGTGGGAACTGGGCTAAGGTTTGAATTGTc
20	S45	489 AGTCCTGGCGGCTTGCCCTACTATTCCATGTGGGAACTGGGCTAAGGTTCTGAATTGTG
25	US6	489 AGTCCTGGCGGCTTGCCCTACTATTCCATGTGGGAACTGGGCTAAGGTTCTGAATTGTG
13	HK4	489 AGTCCTaGCGGCTTGCTTACTATTCCATGTGGGAACTGGGcCAAGGTTTGAATTGTG
18	P10	489 AGTCCTGGCGGCTTGCCCTACTATTCCATGTGGGAACTGGGCTAAGGTTCTGAATTGTG
19	S9	489 AGTCCTGGCGGCTcGCCTACTATTCCATGTGGGAACTGGGCTAAGGTTTGAATTGTG
9-25	consensus	agTCCTgGCGGCTTGCCtACTATTCcATGgtgGgAACTGGGCTAAGGTTtTgATTGTg

NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF
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FIGURE 1B-10

SEQ ID NO:	Isolate	
11	DK1	550 tTGCTACTCTTTGCGCGCGTTGATGGG
24	T10	550 ATGCTACTCTTTGCGCGCGTTGATGGG
10	D3	550 ATGCTACTCTTTGCTGCGTGCACGGC
9	D1	550 ATGCTACTCTTTGCTGCGGTTGACGGC
14	HK5	550 ATGCTACTCTTTGCGCGCGTTGATGGG
15	HK8	550 ATGCTACTCTTTGCGCGCGTTGATGGG
12	HK3	550 ATGCTACTCTTTGCGCGCGTTGATGGG
23	T3	550 cTGCTACTCTTTGCGCGCGTTGATGGG
22	SW2	550 ATGCTACTCTTTGCTGGCGTTGACGGG
17	IND8	550 ATGCTACTCTTTGCGCGCGTTGACGGG
16	IND5	550 ATGCTACTCTTTGCGCGCGTTGACGGG
21	SA10	550 ATGCTACTCTTTGCGCGCGTTGACGGG
20	S45	550 ATGCTACTCTTTGCGCGCGTTGACGGG
25	US6	550 tTGCTACTCTTTGCGCGCGTTGACGGG
13	HK4	550 ATGCTACTCTTTGCGCGCGTTGACGGG
18	P10	550 ATGCTACTCTTTGCGCGCGTTGACGGa
19	S9	550 ATGCTACTCTTTGCTGGTGTGACGGg
9-25	consensus	atGCTACTCTTTGCGCGCGTTGACGGg

FIGURE 1C-1

SEQ ID NO:	Isolate	
26	T2	1 GCCCAAGTGAGGAACACCAgcccGgTtACATGGTGACTAACGACTGTTCcAATGAGAGCA
27	T4	1 GCaCAAGTGAGGAACACCAcTaaCAGCTACATGGTGACcAACGACTGTTCtAATGACAGCA
28	T9	1 GCCgAAGTGAGGAACACCAcAGTACCAGCTACATGGTGACaAATGACTGTTCcAACGACAGCA
29	US10	1 GtCcAAGTGAAaAACACCAcAGTACCAGCTAtATGGTGACcAATGACTGcTCCaACGACAGCA
26-29	consensus	GcccAAGTGAagAACACCAgtacCaGcTAcATGGTGACcAA - GACTGtTCcAA - GAcAGCA
SEQ ID NO:	Isolate	
26	T2	62 TCACcTGGCAGCTCCaAGCCGCGGTtCTCCACGTCCCCGGGTGTaTCCCGTGTGAGAggct
27	T4	62 TCACtTGGCAGCTCCAGGCGCGGTCTCTCCACGTCCCGGGTGTGTCCCGTGGAGAAaac
28	T9	62 TCACcTGGCAACTCCAGGCGCGGTCTCTCCACGTCCCCGGGTGcGTCCCGTGGAGAGAGT
29	US10	62 TCACtTGGCAACTtgAGGctGCGGTCTCTCCACGTtCCCCGGGTGTGTCCCGTGGAGAAAGT
26-29	consensus	TCAC - TGGCA - CTccAgCcGCGGTcCTCCACGTcCCCCGGGTGTgTCCCGTGGcGAGA - agt
SEQ ID NO:	Isolate	
26	T2	123 GGGAAATACATCcCGaTGCTGGATACCGGTcaCACCAAAACGTGGCCGTGGCGGAGCCCGGC
27	T4	123 GGGAAATACATCtCGGTGTGGATACCGGTtTCACCAAAACGTGGCCGTGGCGGAGCCCGGC
28	T9	123 tGGAAAcgCgTCgCGGTGTGGATACCGGTCTCgCCAAACGTaGcGTGCAGCGGCCTGGC
29	US10	123 gGGAAAtaCaTCTcCGGTGTGGATACCGGTCTCaCCAAAtGTgGccGTGCAGCGGCCTGGC
26-29	consensus	gGGAAAtaCaTCTcCGGTGTGGATACCGGTtCaCCAAAcGTgGccGTGC - GC - GCC - GGC

FIGURE 1C-2

SEQ ID NO:	Isolate	
26	T2	184 GCTCTTACGCAGGGCTTGCGGACGCACATcGACATGGTTGTGATGTCCGCCACGCTCTGCT
27	T4	184 GCCCTACGCAGGGCTTGCGGACGCACATtGACATGGTTGTGATGTCCGCCACGCTCTGCT
28	T9	184 GCCCTACGCAGGGCTTGCGGACGCACATCGACATGGTTGTGATGTCCGCCACGCTCTGCT
29	US10	184 GCCCTACGCAGGGCTTGCGGACTcACATCGACATGGTcGTGATGTCCGCCACGCTCTGCT
26-29	consensus	GCcCTcACGCAGGGCTTGCGGACgCACATcGACATGGTtGTGATGTCCGCCACGCTCTGCT
26	T2	245 CTGCCcCTcTACGTGGGGGACCTCTCGCGCGGGGTGATGTCTCGCAGCCAGATGTTcATtGT
27	T4	245 CTGCTCTtTACGTGGGGGACCTCTCGCGCGGGGTGATGTCTCGCAGCCAGATGTTcATcGT
28	T9	245 CCGCTCTcTACGTGGGGGAtCTCTCGCGCGGGGTaATGTCTCGCcGCTcCAGATGTTcATTaT
29	US10	245 CCGCTCTtTACGTGGGGGActTCTGCGGtGGGaTgATGTCTCGCaGCCcCAaATGTTcATTgT
26-29	consensus	C-GCTCT-TACGTGGGGGAccTCTGCGGcGGGgTgATGTCTCGCaGCCcCAGATGTTcATtGt
26	T2	306 CTCGCCGcGACgcCACTGGTTTGTGCAAGAA TGCAATTGCTCcATCTACCCcGGtACCATC
27	T4	306 CTCGCCGCAACAtcACTGGTTTGTGCAAGAcTGCAATTGCTcTATCTACCCtGGcACCATC
28	T9	306 CTCGCCGcAgCACCACTGGTTTGTGcAGGAATGCAACTGCTCCATtTACCCtGGTACCATC
29	US10	306 CTCGCCGcGcCACCACTcGTTTGTGcAGGAATGCAACTGCTCCATcTACCCcGGTACCATC
26-29	consensus	CTCGCCGC-aCacCACTgGTTTGTGCA-GAA TGCAA-TGCTCcATcTACCC-GGtACCATC

FIGURE 1C-3

SEQ ID NO:	Isolate	
26	T2	367 ACTGGACACCGTATGGCATGGGACATGATGATGAACCTGGTCGCCACaGCCACCATGATCC
27	T4	367 ACTGGACACCGTATGGCATGGGATATGATGATGAACCTGGTCGCCACgGCCACCATGATCC
28	T9	367 ACTGGACACCGTATGGCATGGGACATGATGATGAACCTGGTCGCCACaCCACCATGATCt
29	US10	367 ACcGGgCACCGTATGGCATGGGACATGATGATGAACCTGGTCGCCACgCCACcttTGATCC
26-29	consensus	ActGGaCACCGTATGGCATGGGACATGATGATGAACCTGGTCGCCAC - gCCACcaTGATCC
SEQ ID NO:	Isolate	
26	T2	428 TGGCGTACGCGATGCGCGTTCCCGAGGTCAATCaTAGACATCaTcgCGGGGGctCACTGGGG
27	T4	428 TGGCGTACGCGATGCGCGTTCCCGAGGTCAATctTAGACATCgtLAgCGGGGCaCACTGGGG
28	T9	428 TGGCGTACGCGATGCGCGTTCCCGAGGTCAATCaTAGACATCaTcAGCGGaGctCACTGGGG
29	US10	428 TGGCGTACGtGATGCGCGTTCCCGAGGTCAATCaTAGACATCaTtAGCGGgGcGcACtTGGGG
26-29	consensus	TGGCGTACGcGATGCGCGTTCCCGAGGTCAATCaTAGACATCaT - aGCGGgGctCACTGGGG
SEQ ID NO:	Isolate	
26	T2	489 CGTCATGTTtGGCTTGGCCTACTTCTCTATGCAGGAGCGTGGCGGAaGTcaTTGTcATC
27	T4	489 CGTCATGTTcGGCTTGGCCTACTTCTCTATGCAGGAGCGTGGCGGAaGTcGTtGTcATC
28	T9	489 CGTCATGTTcGGCcTAGCCTACTTCTCTATGCAGGAGCGTGGCGGAaGTcGTtGTcATC
29	US10	489 CGTctTGTTcGGctTAGCCTACTTCTCTATGCAGGAGCGTGGCGGAaGTcGTtGTcATC
26-29	consensus	CGTCaTGTTcGGctT - GCCTACTTCTCTATGCAGGAGCGTGGCGGAa - GTcgtTTGTcATC

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FIGURE 1C-4

SEQ ID NO:	Isolate	
26	T2	550 CTctTGCTGGctGCTGGGGTGGACGCG
27	T4	550 CTtcTGCTGGCCGCTGGGGTGGACGCG
28	T9	550 CTgtTGCTcaCCGCTGGcGTGGACGCG
29	US10	550 CTtcTGCTagCCGCTGGgGTGGACGCG
26-29	consensus	CTt-TGCTggCCGCTGGgGTGGACGCG

FIGURE 1D-1

SEQ ID NO:	Isolate	
33	T8	
30	DK8	1 GTGGAAGTtAGaAACacCAGTtttAGCTACTACGCCACCAATGATTGCTGtAAcAACAGCA
32	SW3	1 GTGGAAGTCAGGAACATCAGTTCcAGCTACTACGCCACCAATGATTGCTCAAAcAACAGCA
31	DK11	1 GTGGAAGTCAGGAACATCAGTTCtAGCTACTAtGCCACCAATGATTGCTCAAAcAGCAGCA
30-33	consensus	1 GTGGAAGTCAGGAACacCAGTTCtAGtTACTAcGCCACCAATGATTGCTCAAAcAaCAGCA GTGGAAGTCAGGAACA - CAGTTCtAGcTACTAcGCCACCAATGATTGCTCAAAcAaCAGCA
33	T8	
30	DK8	62 TCACCTGGCAGcTCACCaACGCAGTtCTCCACCTTCCCGGATGCGTCCCATGTGAGAATGA
32	SW3	62 TCACCTGGCAACTCACcGACCGAGTtCTCCACCTTCCCGGATGCGTCCCATGTGAGAATGA
31	DK11	62 TCACCTGGCAACTCACCAACGCAGTcCTCCACCTTCCCGGATGCGTCCCGTGTGAGAATGA
30-33	consensus	62 TCACCTGGCAACTCACCAACGCAGTtCTCCACCTTCCCGGATGCGTCCCaTGTGAGAATGA TCACCTGGCAaCTCACCaACGCAGTtCTCCACCTTCCCGGATGCGTCCCaTGTGAGAATGA
33	T8	
30	DK8	123 CAATGGCACcctTGGCTGCTGGATACAAGTaACACCTaATGTGGCTGTGAaACACCGtGGC
32	SW3	123 CAATGGCACcCTGGCTGCTGGATACAAGTGACACCTaATGTGGCTGTGAaACACCGCGGC
31	DK11	123 tAATGGCACcCTGCACtGCTGGATACAAGTGACACCTaATGTGGCTGTGAaACACCGCGGC
30-33	consensus	123 cAATGGCACcCTGCACtGCTGGATACAAGTGACACCTaATGTGGCTGTGAaACACCGCGGC cAATGGCACCCtTGC - CTGCTGGATACAAGTgACACCTaATGTGGCTGTGAaACACCGcGGC

SEQ ID NO:	Isolate	
33	T8	184 GCACCTCACTCAACCTGCGAAGCgCatGTGACGTGATCGTAATGGCAGCTACGGTCTGCT
30	DK8	184 GCACCTCACTCAACCTGCGAAGCgCatGTGACGTGATCGTAATGGCAGCTACGGTCTGCT
32	SW3	184 GCgCTCACTCAACCTGCGAGCACACGTGATATGATCGTAATGGCAGCTACGGTCTGCT
31	DK11	184 GCaCTCACTCAACCTGCGAGCACaTaGATATGATtGTAATGGCAGCTACGGTCTGCT
30-33	consensus	GCACCTCACTCAACCTGCGA - CaCA - gTcGA -- TGATcGTAATGGCAGCTACGGTCTGCT
33	T8	245 CGGCCTTGATGTGGGgGACGTgTGCGGGGCCGTGATGATaGcGTGCGAGGCTtTCATAAT
30	DK8	245 CGGCCTTGATGTGGGAGACGTaTGCGGGGCCGTGATGATCGTGTGCGAGGCTcTCATAAT
32	SW3	245 CGGCCTTGATGTGGGAGACaTgTGCGGGGCCGTGATGATCGTGTGCGAGGCTtTCATAAT
31	DK11	245 CGGCCTTGATGTGGGAGACgTgTGCGGGGCCGTGATGATCGTGTGCGAGGCTtTCATAgT
30-33	consensus	CGGCCTTGATGTGGGaGACgTgTGCGGGGCCGTGATGATcGtGTGCGAGGCTtTCATAaT
33	T8	306 ATGCCCaGAAAGCCaCAACTTcACCCAGGAGTGCAACTGTTCCATCTACCAAGGTcATATC
30	DK8	306 ATCGCctGAACGCCaCAACTTTACCCAGGAGTGCAACTGTTCCATCTACCAAGGTcATATC
32	SW3	306 ATCGCCAGAAAGCCaCAACTTTACCCaAGAGTGCAACTGTTCCATCTACCAAGGTcGTATC
31	DK11	306 ATCGCCAGAAACaCCACaCACTTTACCCaAGAGTGCAACTGTTCCATCTACCAAGGTcCaATC
30-33	consensus	ATGCCCaGAAAGCCaCAACTTtACCCa - GAGTGCAACTGTTCCATCTACCAAGGTcATATC

FIGURE 1D-3

<u>SEQ ID NO:</u>	<u>Isolate</u>	
33	T8	367 ACCGGCCACCGCATGGCATGGACATGATGCTgAACTGGTCACCAACTCTcACCATGATCC
30	DK8	367 ACCGGCCACCGCATGGCATGGACATGATGCTAAACTGGTCACCAACTCTTACCATGATCC
32	SW3	367 ACCGGCCACCGCATGGCgTGGGACATGATGCTAAACTGGTCACCAACTCTTACCATGATCC
31	DK11	367 ACCGGCCACCGCATGGCaTGGGACATGATGCTtAACTGGTCACCAACTCTcACCATGATCC
30-33	consensus	ACCGGCCACCGCATGGCaTGGGACATGATGCTaAACTGGTCACCAACTCT - ACCATGATCC
33	T8	428 TCGCCTAcGcTcGTGTgCCTGAaCTAGtCCTtgAaGTTGTCTTcGGCGGCCcATTGGGG
30	DK8	428 TCGCCTATGCCGCTCGTGTTCCTGAGCTAGcCCTccAgTTGTCTTcGGCGGCCcATTGGGG
32	SW3	428 TcGCCTATGCCGCTCGTGTTCCTGAGCTAGTcCTTGAAGTTGTCTTcGGCGGCCcATTGGGG
31	DK11	428 TcGCCTATGCCGcCcGTGTTCCTGAGCTAGTCCTTGAAGTcGTCTTcGGTGGtCATTTGGGG
30-33	consensus	TcGCCTATGCCGcTcGTGTtCCTGAGCTAGtCCTtgAaGTTGTCTTcGGCGGCCcATTGGGG
33	T8	489 CGTGGTGTtTGGCTTGGCCtATtTCTCCATGCaAGAGCGTGGGCCAAAGTCATcGCCATC
30	DK8	489 CGTGGTGTtTGGCTTGGCCtATtTCTCCATGCaAGAGCGTGGGCCAAAGTCATtGCCATC
32	SW3	489 CGTGGTGTtTGGCTTGGCCtATtTCTCCATGCaAGAGCGTGGGCCAAAGTCATtGCCATC
31	DK11	489 tGTGGTGTtTGGCTTGGCCtATtTCTCCATGCaAGAGCGTGGGCCAAAGTCATtGCCATC
30-33	consensus	CGTGGTGTtTGGCTTGGCCtATtTCTCCATGCa - GGAGCGTGGGCCAA - GTCATtGCCATC

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FIGURE 1D-4

SEQ ID NO:	Isolate	
33	T8	550 CTCCTcCTTGTcGCAGGAGTGGAcGCA
30	DK8	550 CTCCTtCTTGTcGCAGGAGTGGATGCA
32	SW3	550 CTCCTgCTTGTcGCAGGAGTGGATGCA
31	DK11	550 CTCCTtCTTGTaGCAGGAGTGGATGCA
30-33	consensus	CTCCTtCTTGTcGCAGGAGTGGatGCA

SEQ ID NO:	Isolate
35	DK12
36	HK10
37	S2
39	S54
38	S52
35-39	consensus
62	DK12
62	HK10
62	S2
62	S54
62	S52
35-39	consensus

1	tTAGAGTGGCGGAATGTGTCCGGCCTCTAcGTCCCTTACCAACGACTGTtCCAATAGCAGTA
1	CTAGAGTGGCGGAATGTGTCTGGCCTCTATGTCTTACCAACGACTGTcCCAATAGCAGTA
1	CTAGAGTGGCGGAATACGTCTGGCCTCTATGTCTcACCAACGACTGTTCCAATAGCAGTA
1	CTAGAGTGGCGGAATACGTCTGGCCTCTATaTCCTTACCAACGACTGTTCCAATAGCAGTA
1	CTAGAGTGGCGGAATACGTCTGGCCTCTATgtTCCTTACCAACGACTGTTCCAATAGCAGTA
	cTAGAGTGGCGGAATacGTCTcGGCCTCTAtgtTCCTtACCAACGACTGTtCCAATAGCAGTA
62	TcGTGTATGAGGCCGATGACGTCAttCTGCACACACCTGGCTGTGTACCTTGTGTTCAGGA
62	TTGTGTATGAGGCCGATGACGTCAttCTGCACACACCTGGCTGTGTACCTTGTGTTCAGGA
62	TTGTGTATGAGGCCGATGACGTtAttCTGCACACACCTGGCTGTGTACCTTGTGTTCAGGA
62	TTGTGTATGAGGCCGATGACGTCAttCTGCACACACCGGGCTGTGTACCTTGTGTTCAGGA
62	TTGTGTATGAGGCCGATGACGTCAttCTGCACACACCGGGCTGTGTACCTTGTGTTCAGGA
62	TTGTGTATGAGGCCGATGACGTCAttCTGCACACACCGGGCTGTGTACCTTGTGTTCAGGA
	TtGTGTATGAGGCCGATGACGTCAttCTGCACACACCTGGCTGTGTACCTTGTGTTCAGGA

FIGURE 1E-2

SEQ ID NO:	Isolate	
35	DK12	123 CGGCAATACATctACGTGCTGGACCTCaGTGACgCCTACAGTGGCAGTCAGGTACGTCCGA
36	HK10	123 CGGCAATACATCCACGTGCTGGACCTcGTGACACCTACAGTGGCAGTCAGGTACGTCCGA
37	S2	123 CGGtAATACATCCACGTGCTGGACCCcAGTGACACCTACAGTGGCAGTCAGGTATGTCCGA
39	S54	123 CGGCAATACATCCACGTGCTGGACCCcAGTGACACCTACAGTGGCAGTCAGGTACGTCCGA
38	S52	123 CGGCAATACATCCAtGTGCTGGACCCcAGTGACACCTACAGTGGCAGTCAGGTACGTCCGA
35-39	consensus	CGGcAATACATCcAcGTGCTGGACCCcCaGTGACaCCTACaGTGGCAGTCAGGTACGTCCGA
35	DK12	184 GCAACCAACCGctTCGATACGCAGTCATGTGGACCTGctTAGTGGCGCGGCCcACGATGTGCT
36	HK10	184 GCAACCAACCGCctTCGATACGCAGTCATGTGGACCTGTtTAGTGGCGCGGCCcACGATGTGCT
37	S2	184 GCAACCAACCGCTTCGATACGCAGTCATGTGGACCTATtGTGGCGCGGCCcACtATGTGCT
39	S54	184 GCAACCAACCGCTTCGATACGCAGTCATGTGGACCTATtTAGTGGCGCGGCCcACGCTGTGCT
38	S52	184 GCAACCAACCGCTTCGATACGCAGTCATGTGGACCTATTtTAGTGGCGCGGCCcACGCTGTGCT
35-39	consensus	GCAACCAACCGctTCGATACGCAGTCATGTGGACCTatTaGTGGCGCGGCCcACgatGTGCT

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FIGURE 1E-3

SEQ ID NO:	Isolate	
35	DK12	245 CTGCGCTCTACGTGGGtGATgTGTGTGGGGCCGTCTTCTtGTGGACAAGCCCTTCACGTT
36	HK10	245 CTGCGCTCTACGTGGGcGATATGTGTGGGGCCGTCTTCTCGTGGACAAGCCCTTCACGTT
37	S2	245 CTGCGCTCTACGTGGGTGAATGTGTGGGGCCGTCTTCTCGTGGACAAGCCCTTCACGTT
39	S54	245 CTGCGCTCTATGTGGGTGATATGTGTGGGGCCGTCTTCTCGTGGACAAGCCCTTCACGTT
38	S52	245 CTGCGCTCTATGTGGGTGATATGTGTGGGGCCGTCTTCTCGTGGACAAGCCCTTCACGTT
35-39	consensus	CTGCGCTCTAcGTGGGtGATaTGTGTGGGGCCGTCTTtCTcGTGGACAAGCCCTTCACGTT
35	DK12	306 CAGACctCGTCGCCCATCAAACaGTCCAGACCTGTAACTGCTCGCTGTACCCAGGCCAtCTT
36	HK10	306 CAGACcgcGTGCCCATCAAACGGTCCAGACCTGTAACTGCTCGCTGTACCCAGGCCAcCTT
37	S2	306 CAGACCTCGTCGCCCATCAAACGGTCCAGACCTGTAACTGCTCGCTGTACCCAGGCCATCTT
39	S54	306 CAGACCTCGTCGCCCATCAAACGGTCCAGACCTGTAACTGCTCGCTGTACCCAGGCCATCTT
38	S52	306 CAGACCTCGTCGCCCATCAAACGGTCCAGACCTGTAACTGCTCGCTGTACCCAGGCCATgTT
35-39	consensus	CAGACctCGTCGCCCATCAAACgGTCCAGACCTGTAACTGCTCGCTGTACCCAGGCCAtcTT

NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF
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FIGURE 1E-4

SEQ ID NO:	Isolate	
35	DK12	367 TCAGGACATCGAATGGCTTGGGATATGATGATGAATTGGTCCCCCGCtGTGGGTATGGTGG
36	HK10	367 TCAGGACATCGAATGGCTTGGGATATGATGATGAATTGGTCCCCCGCcGTGGGTATGGTGG
37	S2	367 TCAGGACATCGcATGGCTTGGGATATGATGATGAATTGGTCCCCCGCTGTGGGTATGGTGG
39	S54	367 TCAGGACATCGAATGGCTTGGGATATGATGATGAATTGGTCCCCCGCTGTGGGTATGGTGG
38	S52	367 TCAGGACATCGAATGGCTTGGGATATGATGATGAATTGGTCCCCCGCTGTGGGTATGGTGG
35-39	consensus	TCAGGACATCGaATGGCTTGGGATATGATGATGAATTGGTCCCCCGCtGTGGGTATGGTGG
428	DK12	TagCGCACGTCCTGCGTcTGCCCCCAGACCTTGTTCGACATAATAGctGGGGCCCCATTGGGG
428	HK10	TGGCGCACGTCCTGCGgTTGCCCCCAGACCTTGTTCGACATAATAGCCGGGGCCCCATTGGGG
428	S2	TGGCGCACGTCCTGCGTtTGCCCCCAGACCGTGTTTCGACATAATAGCCGGGGCCCCATTGGGG
428	S54	TGGCGCACATCCTGCGATTGCCCCCAGACCTTGTTCGACATACTGGCCGGGGCCCCATTGGGG
428	S52	TGGCGCACATCCTGCGATTGCCCCCAGACCTTGTTCGACATACTGGCCGGGGCCCCATTGGGG
35-39	consensus	TgGGCGACgTcCTGGCG-tTGCCCCCAGACCTTGTTCGACATAaTaGccGGGGCCCCATTGGGG

NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF
THE ENVELOPE 1...

Bukh et al.

Appl. No.: 09/084,691 Atty Docket: NIH240.1CPDV1
REPLACEMENT SHEET

FIGURE 1E-5

SEQ ID NO:	Isolate	
35	DK12	489 CATCaTGGCGGGCCTAGCCTATTACTCCATGCAGGGCAACTGGGGCAAGGTCGCTATCATC
36	HK10	489 CATCTTGGCaGGCCTAGCCTATTACTCCATGCAGGGCAACTGGGGCAAGGTCGCTATCATC
37	S2	489 CATCTTGGCGGGCCTAGCCTATTACTCCATGCAaGGCAACTGGGGCAAGGTCGCTATCATC
39	S54	489 CATCTTGGCGGGCCTAGCCTATTATTCTATGCAGGGCAACTGGGGCAAGGTCGCTATCATC
38	S52	489 CATCTTGGCGGGCCTAGCCTATTATTCTATGCAGGGCAACTGGGGCAAGGTCGCTATtGTC
35-39	consensus	CATCtTGGCgGGCCTAGCCTATTAcTcATGCAGGGCAACTGGGGCAAGGTCGCTATcaTc
550	DK12	ATGGTTATGTTTTTCAGGaGTCGATGCC
550	HK10	ATGGTTATGTTTTTCAGGGGTcGATGCC
550	S2	ATGGTTATGTTTTTCAGGGGTcGAcGCC
550	S54	ATGATTATGTTTTTCAGGGGTcGATGCC
550	S52	ATGATTATGTTTTTCAGGGGTcGATGCC
550	consensus	ATGgTTATGTTTTTCAGGgGTCGAtGCC

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FIGURE 1F-1

[illegible]

FIGURE 1F-2

<u>SEQ ID NO:</u> 43	<u>Isolate</u> Z7	306 CCAGCCGGCAGCCCACTGGACTAGCAGGACTGCAATTGTTCCATCTATGCgGGGCAgTt
42	Z6	306 CCAGCCGGCAGCCCACTGGACTAGCAGGACTGCAATTGTTCTATCTAGCAGGGCATATC
42-43 consensus (Z6)		CCAGCCGGCAGCCCACTGGACTAGCAGGACTGCAATTGTTCTATCTAGCAGGGCAaTc
<u>SEQ ID NO:</u> 43	<u>Isolate</u> Z7	367 ACaGGCCACAGaATGGCATGGACATGATGAACTGGAGTCCCAACCAcCtTgTCC
42	Z6	367 ACgGGCCACAGgATGGCATGGACATGATGAACCTGGAGTCCCAACCAcCCTGcTtC
42-43 consensus (Z6)		ACgGGCCACAGgATGGCATGGACATGATGAACCTGGAGTCCCAACCAcCCTGcTtC
<u>SEQ ID NO:</u> 43	<u>Isolate</u> Z7	428 TCGCCcAGGTtATGAGGATCCCTAGCACTCTGGTgGACCTACTCaCTGGAGGGCACTGGGG
42	Z6	428 TCGCCcAGGTtATGAGGATCCCTAGCACTCTGGTgGATCTACTCGCTGGAGGGCACTGGGG
42-43 consensus (Z6)		TCGCCcAGGTtATGAGGATCCCTAGCACTCTGGTgGATCTACTCGCTGGAGGGCACTGGGG
<u>SEQ ID NO:</u> 43	<u>Isolate</u> Z7	489 taTCCTTaTcGGGgTGGCaTACTTctGCATGCAAGCTAAATGGGCCAAGGTCAtCTGGTC
42	Z6	489 CgTCCTTgTTGGGtTGGCGTACTTCAGtATGCAAGCTAAATGGGCCCAaGTCACTCTGGTC
42-43 consensus (Z6)		cgTCCTTgTtGGGtTGGCGTACTTCaGtATGCAAGCTAAATGGGCCCAaGTCACTCTGGTC
<u>SEQ ID NO:</u> 43	<u>Isolate</u> Z7	550 CTTTTCTCTaCGCTGGAGTTGATGCC
42	Z6	550 CTTTTCTCTtCGCTGGAGTTGATGCC
42-43 consensus (Z6)		CTTTTTCTCTtCGCTGGAGTTGATGCC

FIGURE 1G-1

SEQ ID NO:	Isolate	
45	SA1	1 GTtCCCTACCGgAATGCCTCTGGGGTTTAcCATGTcACCAATGAcTGCCCCAAACTCcTCCA
47	SA5	1 GTCCCTACCGAAATGCCCTCTGGGGTTTATCATGTcACCAATGAATGCCCAAACTCTTCCA
49	SA7	1 GTCCCTACCGAAATGCCCTCcGGGGTTTATCATGTcACCAATGAATGCCCGAACTCTTCCA
46	SA4	1 GTTCCCTACCGAAAcGCCCTCTGGGGTTTATCATGTcACCAATGAATGCCCAAACTCTTCCA
50	SA13	1 GTTCCCTACCGAAATGCCCTCTGGGGTTTATCATGTcACCAATGAATGCCCAAACTCTTCCA
48	SA6	1 GTTCCtTACCGgAATGCCTCTGGGGTgTATCATGTtACCAATGAATGCCCAAACTCTTCCA
45-50	consensus	GTtCCcTACCGgAATGCCTCtGGGGTtTATcATGTcACCAATGAATGCCCAAACTCtTCCA
SEQ ID NO:	Isolate	
45	SA1	62 TAGTCTACGAGGCTGATAgCCTGATctTGcACGCACcCTGGcTGCGTGCCCTGTGTcAGGcA
47	SA5	62 TAGTCTACGAGGCTGATAAcCTGATtCTGcACGCACcCTGGTTGCGTGCCCTGTGTcAaGgA
49	SA7	62 TAGTCTAtGAGGCTGAcAAcCTGATCCTTGcACGCACcCTGGTTGCGTGCCCTGTGTcAGaCA
46	SA4	62 TAGTtTACGAGGCTGATAAcCTGATCTTGcATGCACcCTGGTTGCGTGCCcTGTGTcAGGCA
50	SA13	62 TcGTCTACGAGGCTGATGACCTGATCTTAcACGCACcCTGGTTGCGTGCCCTGTGTtAGGCA
48	SA6	62 TagTCTAtGAGGCTGATGACCTGATCcTAcACGCACcCTGGcTGCGTGCCCTGTGTtccGGaA
45-50	consensus	TagTcTAcGAGGCTGATaaCCTGATc-TgCacGCACcCTGGtTGCGTGCCcTGTGTcaggcA

FIGURE 1G-2

SEQ ID NO:	Isolate	
45	SA1	123 AGaTAATGTCAGTAGGTGCTGGGTCCAAATCACCCCCACAcTGTAGCCCCGAGAcCtTCGGA
47	SA5	123 AGgTAATGTCAGTAGGTGCTGGGTCCAAATCACCCCCACAcTGTAGCCCCGAGAcCtTCGGA
49	SA7	123 AaATAATGTCAGTAGGTGCTGGGTCCAAATCACCCCCACAcTGTAGCCCCGAGAcCtTCGGA
46	SA4	123 AGaTAATGTCAGTAaGTGCTGGGTCCAAATCACCCCCACgTTGTAGCCCCGAGAcCtTCGGA
50	SA13	123 GGgTAATGTCAGTAGGTGCTGGGTCCAgATCACCCCCACAcTGTAGCCCCGAGAcCtTCGGA
48	SA6	123 GGaTAATGTCAGTAGaTGCTGGGTtCAATCACCCCCACACTaTCAGCCCCGAGAcCtTCGGA
45-50	consensus	agaTAATGTCAGTAGgTGCTGGGTcCAaATCACCCCCACa -TgTCAGCCCCGAGAcCtTCGGA
45	SA1	184 GCGGTACGGCTCCTCTTCGGAGGGcCGTTGACTACTTAGCGGGAGGaGCTGCTCTCTGCT
47	SA5	184 GCGGTACGGCTCCTCTTCGGAGGGtCGTTGACTACTTAGCGGGAGGGGCTGCCCTCTGCT
49	SA7	184 GCGGTACGGCTCCTCTTCGGAGGGCCGTTGACTACcTAGCGGGAGGGGCTGCCCTCTGCT
46	SA4	184 GCGGTACGGCTCCTCTTCGGAGGGCCGTTGACTACTTAGCGGGAGGGGCTGCCCTCTGCT
50	SA13	184 GCGGTACGGCTCCTCTTCGGAGGGCCGTTGACTACTTAGCGGGAGGGGCTGCCCTtTGCT
48	SA6	184 GCGGTACGGCTCCTCTTCGGAGGGCCGTTGATtTACTTgCGGGaGGGGCCGCCCTtTGCT
45-50	consensus	GCGGTACGGCTCCTCTTCGGAGGGcCGTTGAcTACTaTCGGGGaGGGgGtGCcCtTcTGCT

SEQ. ID NO.:	Isolate	
45	SA1	245 CCGCACTATACGTCCGcGACCGTGCgGGGCAGTGTtctTGGTAGGCCAAATGTTCAcCTA
47	SA5	245 CCGCACTATACGTCCGgGACCGTGCgGGGCAGTGTtctTGGTAGGCCAAATGTTCAcCTA
49	SA7	245 CCGCgCTATACGTCCGgGACCGTGCgGGGCAGTGTtTTTGGTAGGCCAgATGTTCAgCTA
46	SA4	245 CCGCaCTATACGTCCGgGACCGTGCgGGGCAGTGTtTTTGGTAGGCCAAATGTTCAcCTA
50	SA13	245 CCGCGTTATACGTCCGAGACCGTGCgGGGCAGTGTtTTTGGTAGGTCAAATGTTCAcCTA
48	SA6	245 CCGCGTTATACGTCCGAGACGtGTGCgGGGCAT-TGTtTTTGGTAGGcCAAATGTTCAcCTA
45-50	consensus	CCGC- cTATA CGTCCGgGACGcGTGCgGGGCAGTGTtTtTGGTAGGcCaaATGTTCAcCTA
SEQ. ID NO.:	Isolate	
45	SA1	306 TAGGCCTGCCAGCATAcCaGTGCAGGACTGCAACTGTtCCATTTACAGtGGCCATATC
47	SA5	306 TAGGCCTGCCAGCATACTACGGTGCAGGACTGCAACTGTtCCATTTACAGcGGCCATATC
49	SA7	306 TAGGCCTGCCAGCACACTACGGTGCAGGACTGCAACTGTtCCATTTACAGTGGCCATATC
46	SA4	306 TAGGCCTGCCAGCACACTACGGTGCaaGACTGCAAtTgcTctATTTACAGTGGCCATATC
50	SA13	306 TAGcCCTGCCCGCATAaTgttGTGCAGGACTGCAACTGtTCCATTTACAGTGGCCAcATC
48	SA6	306 TAGgCCTGCCCaGCAtgctAcgGTaCAGGACTGCAACTGcTCCATTTACAGTGGCCAtATC
45-50	consensus	TAGgCCTGCCCaGCAactacgGTgCAGGACTGCAAcTGtTccATTTACAGtGGCCAtATC

FIGURE 1G-4

<u>SEQ ID NO:</u>	<u>Isolate</u>
45	SA1
47	SA5
49	SA7
46	SA4
50	SA13
48	SA6
45-50	consensus
367	ACCGGCCACCGgATGGcTtGGGACATGATGAATTGGTCACCTACGACAGCCTTGcTGA
367	ACCGGCCACCGAATGGcATGGGACATGATGAATTGGTCACCTACGACAGCCTTGcTGA
367	ACCGGCCACCGAATGGcATGGGACATGATGAATTGGTCACCTACGACAGCCTTGcTGA
367	ACCGGCCACCGGATGGcATGGGACATGATGAATTGGTCACCTACGACgGCCTTGcTGA
367	ACCGGCCACCGGATGGcATGGGACATGATGAATTGGTCACCTACaACAGcTtTGGTGA
367	AcTGGCCACCGGATGGcATGGGACATGATGAATTGGTCACCCcgCgACAGCcTtTGGTGA
428	TGGCCCCAGaTGCTACGGATcCCCCAGtGGTCATaGACATCATaGCCGGGGGCCACTGGGG
428	TGGCCCCAGgTGCTACGGATTCCCCAaGTGGTCATtGACATCATtGCCGGGGGCCACTGGGG
428	TGGCCCCAGtTGCTACGGATTCCCCAGTGGTCATCGACATCATtGCCGGGGGCCACTGGGG
428	TGGCCCCAGtTGCTACGGATTCCCCAGTGGTCATCGACATCATtGCCGGGGGCCACTGGGG
428	TGGCCCCAGtTGtTACGGATTCCCCAGTGGTCATtGACATCATtGCCGGGGCcCCACTGGGG
428	TGGCCCCAaaTGcTACGGATTCCCCAGTGGTCATtGACATCATtGCCGGGGgCCACTGGGG
45-50	TGGCCCCAgTtGcTACGGATtCCCCAGtGGTCATtGACATCATtGCCGGGGgCCACTGGGG
<u>SEQ ID NO:</u>	<u>Isolate</u>
45	SA1
47	SA5
49	SA7
46	SA4
50	SA13
48	SA6
45-50	consensus

NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF
THE ENVELOPE 1...

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Appl. No.: 09/084,691 Atty Docket: NIH240.1CPDV1
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FIGURE 1G-5

SEQ ID NO:	Isolate	
45	SA1	489 GGTCTTGTTtGCCGcCGCATACTTtGGTCgGCCcGCCAACTGGGCTAAGGTaGTGCTGGTt
47	SA5	489 GGTCTTGTTcGCCCGtCGCATACTTCGGTCAGCGGCTAACTGGGCTAAGGTtGTGCTGGTC
49	SA7	489 GGTCTTGTTcGCCCGCGCATAATTTCGGTCAGCGGCTAACTGGGCTAAGGTtGTGCTGGTC
46	SA4	489 GGTCTTGTTtGCCCGCGCATAATTTCGGTCAGCGGCTAACTGGGCTAAGGTtTaCTGGTC
50	SA13	489 GGTCTTGTTcGCCCGCGCATACTaCGCGTCGGCGGCTAACTGGGCTAAGGTtGTGCTGGTC
48	SA6	489 GGTCTTGTTcGCCCGCtGCATACTcCGCGTCGGCGGCTAACTGGGCTAAGGTtGTGCTGGTC
45-50	consensus	GGTCTTGTTcGCCGccGCATACTcCGGTC-GCGGCTAACTGGGCTAAGGTtGTgCTGGTC
45	SA1	550 CTGTTcCTGTTTcCGGGGGTcGATGGC
47	SA5	550 CTGTTCTGTTTcCGGGGGTcGATGGC
49	SA7	550 TTGTTCTGTTTcCGGGGGTcGATGCC
46	SA4	550 TTGTTCTGTTTcCGGGGGTcGATGCC
50	SA13	550 cTGTTCTGTTTcCGGGGGTcGATGCC
48	SA6	550 tTGTTCTGTTTcCGGGGGTtGATGCC
45-50	consensus	-TGTTtCTGTTTcCGGGGGTcGATGcc

FIGURE 1H-1

SEQ ID NO:	Genotype	
30-33	(IV/2b)	1 GTGGAAGTCAGAAACATCAGTTTctAGCTACTAGCCCAATGANTGCTCaAAcAaCAGCA
34	(2c)	1 GTGGAGGTCAAGCAGCACCAGGCGACTCTTACATGCCGACCAACGANTGCTCCAACCTCTAGTA
26-29	(III/2a)	1 GcccAAGTGAaGAAcACCAgtaCaGcTAcATGGTGACCAACGACTGTTCcAATGACAGCA
35-39	(V/3a)	1 cTAGAGTGGCGGAATaCGTctGGCCTCTATgTCTtACCAACGACTGTtCCAATAGCAGTA
9-25	(II/1b)	1 tAtGAaGTGCGCAACGTgTCCGGGgtgTaccAtGTcACGAAcAGACTGTcCCAACtcaAGGa
1-8	(I/1a)	1 tACCAAGTgCGCAACTCcaCgGGgCTtTACCAtGTcACCAATGAtTGCCCTAACTTCGAGtA
40	(4a)	1 GAGCACTACCGGAATGCTTCGGGCATCTACATcACCAATGAtTGTCCGAATtCCAGTA
42-43	(4c)	1 GTtAACTATGcCAATGCCTCGGGCGTCTATcAGTcACCAACGACTGCCCGAACTCGAGCA
44	(4d)	1 TACAACtATGCAACAGCTCGGGTGTCTACCATGTcACCAACGACTGCCCGAACTCGAGCA
41	(4b)	1 GTGCACTACCGGAATGCTTCGGGGCTCTATCATGTcACCAATGAtTGGCCCTAAcACcAGCA
45-50	(5a)	1 GTtCCcTACCGGAAtGCCTctGGGGTtTATCATGTcACCAATGAtTGCCCAAACTctTCCA
51	(6a)	1 CTTACCTACGGCAACTCCAGTGGGCTATACCATCTcACAATGAtTGCCCCAACTCCAGCA
1-51	consensus	A TA AC AA GA TG C AA
SEQ ID NO:	Genotype	
30-33	(IV/2b)	62 TCACCTGGCAaCTCACCaACGCAGTtCTCCACCTTCCCGGATCGTCCCaTGTGAGAATGA
34	(2c)	62 TCGTTTGGCAGCTTGAAGGAGCAGTGTCTTcATACTCTGGATCGTCCCTTGTGAGCGTAC
26-29	(III/2a)	62 TCACcTGGCAaCTcAgGCCcGGGTtCTCCACGTcCCCGGGTgtgTCCCGTGCAGAAagt
35-39	(V/3a)	62 TtGTGTATGAGGCGGATGAGTcATTCTGCACACACcTGGCTGTGTACCTTGTGTTCAGGA
9-25	(II/1b)	62 TtGTGTatGAGGcAgCGGACaTGATcATGCAcACcCCGGGTGcgTgCCCTGcGttCgGGGA
1-8	(I/1a)	62 TtGTGTACGAGcGgCCGATgCcATcCTgCAcaCtCCGGGTGTGTcCCTTGCCTTCGCGGA
40	(4a)	62 TAGTCTATGAAGCTGACCATACATCTCTACCTTCCCGGGTGCCTACCTGTGTGTGATGAC
42-43	(4c)	62 TAGTGTATGAGGCCGAACACCAgATctTACACCTCCAGGTGTCTgCCCTGTGTGAGGGT
44	(4d)	62 TAGTCTATGAaACCGATTACCACTTTACACCTCCCGGATGCGTTCTTGGCTGAGGGA
41	(4b)	62 TAGTGTACGAGACGGAGCACCATCATGCACTTGCCAGGGTGTGTCCCTGTGTGCGGAC
45-50	(5a)	62 TagTcTACGAGGCTGataaCCTGATctTgCAcGCACCTGgtTGCGTGCCctGTGTcaggca
51	(6a)	62 TCGTGTGGAGCGGATGCTATGATCTTGCATTTTGCCTGGATGCTTGGCTTGTGTGAGGGT
1-51	consensus	T A T T CA CC GG TG T CC TG G

<u>SEQ ID NO:</u>	<u>Genotype</u>	
30-33	(IV/2b)	123 CAATGGCACCCcTGCgCTGCTGGATAACAAGtGACACTAATGTGGCTGTGAACAACCGcGGC
34	(2c)	123 CGCCAACGTCTCTCGATGTTGGTGCCGGTTGCCCAATCTGCCATAAGTCAAACCTGGC
26-29	(III/2a)	123 GGGAAAtCaTctCGTGTGGATACCgGTctCaCCAAAcGTgGccGTGaGcCaGCCcGGC
35-39	(V/3a)	123 CGGcAATACATCcAcGTGCTGGACCCcCaGTGACaCCTACaGTGGCAGTCAGTAacGTTCGGA
9-25	(II/1b)	123 gaacAAActcCTCccgcTgcTGGGTaGCGTcaCtCCCACgCTcGCgGccAGGAACgcccAgC
1-8	(I/1a)	123 GGgTaaCgcccCGAggTGTtGGGTGgCGgTgaCCCCACgGTgGCCAccAGGAcGGCAaA
40	(4a)	123 TGGGAACACATCGCGTtGCTGGACGCCGGTGACCGCTACAGTGGCTGTGGCACACACCCGGGG
42-43	(4c)	123 tGGGAATCAGTCACGTCGTGGGTGGCCCTTACTCCACCGTGGCGgtGtCTTATATTCGT
44	(4d)	123 AGGGAACAAGTCTACATGCTGGGTGTCTCTCACCCCCACCGTGGCTGGCAACATCTGAAT
41	(4b)	123 GGAGAATACTTCTCGCTGCTGGGTGCCCTTGACCCCCCATGTGGCCGGCCCTATATCCCAAC
45-50	(5a)	123 agaTAATGTcAGTAGgTGTGGGTcCAaATCACCCCCACatTgTCAGCCCCCGAaccTCGGA
51	(6a)	123 CGATGATCGGTCCACCTGTGGCATGCTGTGACCCCCACCTGGCCATACCAATGCTTTC
1-51	consensus	TG TGG T C CC A T C
1-51	consensus	
30-33	(IV/2b)	184 GCaTcACTCaAACCTGCGAaCaCatgTcGacaTGATcGTAATGGCAGCTACGGTCTGCT
34	(2c)	184 GCTCTCACTAAGGCTTGCAGCACACATCGATATCATCGTGTATGTCTGTACGGTCTGT
26-29	(III/2a)	184 GCCCTcACGcAGGGCTTGGGACgCACATcGACATGGTtGTATGTCCGCCACGCTCTGCT
35-39	(V/3a)	184 GCAACCAcCGCTTCGATACGcAGTCATGTGGACCTatTaGTGGCGCGCGCCACgaTGTGCT
9-25	(II/1b)	184 gTCCcCAcTAcGaCaATACGACgCcAcGTcGATTTGCTCGTTGGGGCGGTgctTTCTGCT
1-8	(I/1a)	184 CTCCCcgCaacCGCagCTcCGACGTcACATCGATcGTGCTGTcGGAGcGCCACCCCTCTGCT
40	(4a)	184 GCTCCGCTTGAGTTCGTTCCGGCGACATGTGGACCTTAATGGTAGGGCGGCCACTTTGTGT
42-43	(4c)	184 GctCCGCTTGAcTCCcTCCGGAGACATGTGGACCTGTATGGTgGGCGccGCTACTgTaTGCT
44	(4d)	184 GCTCCGCTTGAGTCTTTGAGACGTcACGTGGATCTGTATGGTGGCGCGGCCACTCTCTGCT
41	(4b)	184 GCACCGTTAGATCCATGCGCAGGcATGTAGACCTGTATGGTGGGTGCGGTACTATGTGTT
45-50	(5a)	184 GCGGTACGGCTCCTCTTCGGAGGGcCGTTGAcTACTaGCGGgaGGgGCTcGcCTcTGCT
51	(6a)	184 ACGCCCGCAACGGGATTCCGcAGGcATGTGGATCTTCTTGGGGGGCGCGcAGTGGTTTGTCT
1-51	consensus	T G T GA T G T G GC T TG T
1-51	consensus	

SEQ ID NO:	Genotype
30-33	(IV/2b)
34	(2c)
26-29	(III/2a)
35-39	(V/3a)
9-25	(II/1b)
1-8	(I/1a)
40	(4a)
42-43	(4c)
44	(4d)
41	(4b)
45-50	(5a)
51	(6a)
1-51	consensus

306 ATGCGCaGAACgCCACaACtTTtACCCaAGAGTGCAACTGTtTCCATCTACCAAGGTcatATC
306 GTCGCCACAACACCATACGtTTGTCCAGGAATGCAACTGTtTCCATATACCCGGGGCCGcATT
306 CTGCGCGCaACacCACtGtGTTGTGCAAGaATGCAATtTGCTCCaTcTACCCtGGtACCAATC
306 CAGACctCGTCGCCATCAAAcGtTCCAGACCTGTAACTGCTCGCTGTACCCAGGCCcatcTT
306 cTcGcCctCGcCgGcAtgaGACagtaCAGgAcTGcAAcTgCTCaaTCTATCTCCcGGcCagTta
306 cTctCCCAGgGcCaCTGGACaACGCAAGaCTGcAAATGTtTctATCTATCCcGGCCATAta
306 TCGGCGCGGTGCGCACTGGACCAcGcAGGAGTGCAATtGTtTCCATCTACACTGGCCATATc
306 CCAGCGCGACGCGCACTGGACTACGcAGGACTGcAAATGTtTctATCTAcGcAGGGcATaTc
306 CCAACCTCGCGCGCACTGGACCAcCCAGACTGcAAATGTtTCCATCTACACAGGACATATc
306 CCGACCGCGCGCGCACTGGACCAcCCAGGATtTGCAACTGCTCCATCTATCTCGTGGTCAGGTC
306 TAGgCCTCGCCaGCatactacgGTgCAGGACTGcAAcTgTcCaTTTACAGtGGCCATATc
306 TCAGCCCCCGCGTcATTGGACTGTGCAAGACTGcAACTGCTCCATCTATACAGGCCACGTC

FIGURE 1H-4

SEQ ID NO:	Genotype	
30-33	(IV/2b)	367 ACCGGCCACCGCATGGCaTGGACATGATGCTAACTGGTCACCAACTCTtACCAATGATCC
34	(2c)	367 ACGGGACACCGCATGGCTTGGGATATGATGAATGGTGGCCCACTACCAACCATGCTCC
26-29	(III/2a)	367 ActGGaCACCGTATGGCATGGGACATGATGAATGGTGGCCCAcggCCACcaTGATCC
35-39	(V/3a)	367 TCAGGACATCGaATGGCTTGGGATATGATGAATGGTGGCCCGCTGTGGGTATGGTGG
9-25	(II/1b)	367 tCAGGTcAcCGcATGGCTTGGGATATGATGAATGGTGGTCCcCTACaGCaGcCcTaGTg
1-8	(I/1a)	367 ACGGGtCacCGcATGGCaTGGGATATGATGAATGGTGGTGGTCCcCTACaGCaGcCcTaGTg
40	(4a)	367 ACCGGCCACAGGATGGCGTGGGACATGATGAATGGTGGTGGTGGTGGTGGTGGTGGTGG
42-43	(4c)	367 ACgGGCCACAGgATGGCATGGGACATGATGAATGGTGGTGGTGGTGGTGGTGGTGGTGG
44	(4d)	367 ACAGGACACAGAAATGGCTTGGGACATGATGAATGGGAGCCCTACCAACCCcTGcTtC
41	(4b)	367 TCGGGCCACAGGATGGCTTGGGACATGATGAATGGGAGCCCTACCAACCCcTGcTtC
45-50	(5a)	367 ACcGGCCACCGgATGGCaTGGGACATGATGAATGGTGGTGGTGGTGGTGGTGGTGGTGG
51	(6a)	367 ACCGGCCACAGGATGGCTTGGGACATGATGAATGGTGGTGGTGGTGGTGGTGGTGGTGG
1-51	consensus	C GG CA G ATGGC TGGGA ATGATG T AA TGG CC C T T T
SEQ ID NO:	Genotype	
30-33	(IV/2b)	428 TcGCCtATgCCcGCTCGTGTtCCTGAgCTAGtCCtTgAaGtTGTCTTCGGcGGcCATtTGGGG
34	(2c)	428 TGGCGTACTTGGTGGCATCCCGGAAGTCATCTTGGATATGTTACAGGAGGTCAATtTGGGG
26-29	(III/2a)	428 TGGCGTACGcGATGGCGGTtCCCGAGGTcATCaTAGACATCaTtaGCGGgGCTcAcTGGGG
35-39	(V/3a)	428 TgGGcACgTcCTGGCTtTGCCCCAGACCTTGTtCGACATAaTaGcCGGGCCCATtTGGGG
9-25	(II/1b)	428 TaTGGCAGtTaCTCCGgaTCCCaCAAGCTgTcGTGGaCaTGGTgGcGGgGCCACtTGGGG
1-8	(I/1a)	428 TaGctCAGCTGTCTcGGaTCCCGCaAGCCaCTTTGGACaATGATCGCTGGtGcCcCACTTGGGG
40	(4a)	428 TCGCCcAGATCATGAGGGTtCCCCACAGCCtTTCTCGACATGGTtGCCGAGGCCACtTGGGG
42-43	(4c)	428 TCGCCcAGGTcATGAGGATCCCTAGCACTCTGGTaGATCTACTCgCTGGAGGGcACTTGGGG
44	(4d)	428 TCGCCCAACTTATGAGGATCCcAGGCGGCATGGTCCGACCTGTCTTGCAGGGCGGCACtTGGGG
41	(4b)	428 TGGCTCAGATCTTACGGATCCCTCTATCTTAGGTGACTTGTCTCAcCGGGGGTCACTTGGGG
45-50	(5a)	428 TGGCCcAGtTgCTACGGATtCCCCAGTGGTTCATtGACATCATtGCCGGGGgCCACTGGGG
51	(6a)	428 TATCTAGCATCTTgAGGGTACCTGAGATTTGTGGAGTGTGATATTTTGGTGGCCATtTGGGG
1-51	consensus	T C G T CC T T GG G CA TGGGG

FIGURE 1H-5

[illegible]

FIGURE 2A-1

SEQ ID NO:	Isolate	
56	S14	1 YQVRNSTGLYHVTNDCPNSSIVYEaDAAILHaPGCVPCVREGNtSRCWAMtPTVATRDGK
52	DK7	1 YQVRNSTGLYHVTNDCPNSSIVYEaDAAILHTPGCVPCVREGNvSRCWAMtPTVATRDGK
59	US11	1 YQVRNSTGLYHVTNDCPNSSIVYEaDAAILHTPGCVPCVREGNaSRCWAMtPTVATRDGK
55	DR4	1 HQVRNSTGLYHVTNDCPNSSIVYEaDAAILHTPGCVPCVREGNtSRCWAVtPTVATRDGK
54	DR1	1 HQVRNSTGLYHVTNDCPNSSIVYEaDAAILHaPGCVPCVREGNASRCWAVtPTVATRDGK
53	DK9	1 YQVRNSSGLYHVTNDCPNSSIVYEaDAAILHSPGCVPCVREGNASKCWAVAPtVATRDGK
58	SW1	1 YQVRNSSGLYHVTNDCPNSSIVYEaDAAILHSPGCVPCVREGdApKCWAVAPtVATRDGK
57	S18	1 YQVRNSTGLYHVTNDCPNSSIVYEaDtLiLHSPGCVPCVREGnAsrCWVpVAPtVATRDGK
52-59	consensus	YQVRNSTGLYHVTNDCPNSSIVYEaDaAILH- PGCVPCVREGnasrCWVavtPTVATRDGK
56	S14	62 LPatQLRRyIDLLVGSATLCSALYVGDLGCVFLVGLQFTFSPrRLtWTtQdCNCsIYPGHI
52	DK7	62 LPTaQLRRHIDLLVGSATLCSALYVGDLGCVFLVGLQFTFSPrRHWTtQdCNCsIYPGHI
59	US11	62 LPTTQLRRHIDLLVGSATLCSALYVGDLGCVFLVGLQFTFSPrRHWTtQdCNCsIYPGHI
55	DR4	62 LPTTQLRRHIDLLVGSATLCSALYVGDLGCVFLVGLQFTFSPrhWTtQdCNCsIYPGHI
54	DR1	62 LPTTQLRRHIDLLVGSATLCSALYVGDLGCVFLVGLQFTFSPrRHWTtQdCNCsIYPGHI
53	DK9	62 LPATQLRRHIDLLVGSATLCSALYVGDLGCVFLVGLQFTFSPrRHWTtQdCNCsIYPGHI
58	SW1	62 LPATQLRRHIDLLVGSATLCSALYVGDLGCVFLVGLQFTFSPrRHWTtQdCNCsIYPGHI
57	S18	62 LPATQLRRHIDLLVGSATLCSALYVGDLGCVFLVGLQFTiSPRRHWTtQdCNCsIYPGHI
52-59	consensus	LP-tQLRRhIDLLVGSATLCSALYVGDLGCVFLVGLQFTfSPRrhWTtQdCNCsIYPGHI

FIGURE 2A-2

SEQ ID NO:	Isolate		
56	S14	123	TGHRMADMMNWSPTTALVVAQLLRIPQAiLDMiAGAHGVLAGIAYFSMVGNNWAKVLV
52	DK7	123	TGHRMADMMNWSPTTALVVAQLLRIPQAiLDMiAGAHGVLAGIAYFSMVGNNWAKVLV
59	US11	123	TGHRMADMMNWSPTaALVVAQLLRIPQAiLDMiAGAHGVLAGIAYFSMVGNNWAKVLV
55	DR4	123	TGHRMADMMNWSPTTALVVAQLLRIPQAiLDMiAGAHGVLAGIAYFSMVGNNWAKVLV
54	DR1	123	TGHRMADMMNWSPTTALVMAQLLRIPQAiLDMiAGAHGVLAGIAYFSMVGNNWAKVVV
53	DK9	123	TGHRMADMMNWSPTaALVMAQLLRIPQAiLDMiAGAHGVLAGIAYFSMVGNNWAKVVV
58	SW1	123	TGHRMADMMNWSPTTALVvAQLLRIPQAiLDMiAGAHGVLAGIAYFSMVGNNWAKVLiV
57	S18	123	TGHRMADMMNWSPTTALViAQLLRvPQAiLDMiAGAHGVLAGIAYFSMaGNWAKVLiV
52-59	consensus		TGHRMADMMNWSPTTALVvAQLLRiPQAiLDMiAGAHGVLAGIAYFSMVGNNWAKVLvV
SEQ ID NO:	Isolate		
56	S14	184	LLLFAGVDA
52	DK7	184	LLLFAGVDA
59	US11	184	LLLFAGVDA
55	DR4	184	LLLFAGVDA
54	DR1	184	LLLFAGVDA
53	DK9	184	LLLFtGVDA
58	SW1	184	LLLFsGVDA
57	S18	184	LLLFaGVDA
52-59	consensus		LLLFaGVDA

FIGURE 2B-1

SEQ ID NO:	Isolate	
75	T10	1 YEVRNVSGmYHVTNDCSNSSIVFEaAdLIMHTPGVPCVREGNsRCWVALTPTLAARntS
62	DK1	1 YEVRNVSGvYHVTNDCSNSSIVYEaVdVIMHTPGVPCVRENNhSRCWVALTPTLAARNAS
64	HK4	1 hEVhNVSGiYHVTNDCSNSSIVYEaADMIMHTPGVPCVRENNSSRCWVALTPTLAARNAS
76	US6	1 YEVRNVSGmYHVTNDCSNSSIVYEaADMIMHTPGVPCVRENNSSRCWVALTPTLAARNAS
68	IND8	1 YEVRNVSGvYHVTNDCSNSSIVYEaADMIMHTPGVPCVREGNfSSCWVALTPTLAARNAS
67	IND5	1 YEVRNVSGvYHVTNDCSNSSIVYEaADMIMHTPGVPCVREGNSSRCWVALTPTLAARNAS
73	SW2	1 YEVRNVSGvYHVTNDCSNSSIVYETADIMIMHTPGVPCVREaNSSRCWVALTPTLAARntS
63	HK3	1 YEVRNVSGiYHVTNDCSNSSvVYETADIMIMHTPGVPCVRENNSSRCWVALTPTLAARNVS
66	HK8	1 YEVRNVSGiYHVTNDCSNSSIVYETADIMIMHTPGmPCVRENNSSRCWVALTPTLAARNVS
61	D3	1 YEVRNVSGvYqVTNDCSNSSIVYETADIMIMHTPGVPCVREDnSSRCWVALTPTLAARNsS
74	T3	1 YEVRNVSGvYVTNDCSNSSIVYETADIMIMHTPGVPCVRESnSSRCWVALTPTLAARNAS
65	HK5	1 YEVRNVSGvYHVTNDCSNLSIVYETdMIMHTPGVPCVRENNSSRCWVALaPTLAARNAS
71	S45	1 YEVRNVSGaYHVTNDCSNSSIVYEaVdVlIMHTPGVPCVRENNSSRCWVALTPTLAARNSS
72	SA10	1 YEVRNVSGmYHVTNDCSNSSIVYEaADMIMHTPGVPCVRENNSSRCWVALTPTLAARNSS
69	P10	1 YEVRNVSGvYHVTNDCSNSSIVYEaADMIMHTPGVPCVRENNSSRCWVALTPTLAARNSS
60	D1	1 YEVRNVSGvYHVTNDCSNSSIVYEtADMIMHTPGVPCVREDnSSRCWVALTPTLAARNgn
70	S9	1 YEVRNVSGaYHVTNDCSNSSIVYEaAdVIMHTPGVPCVqEgNSSqCWVALTPTLAARNat
60-76	consensus	YEVRNVSGvYhVTNDCSNSSiVYEEaDmImHTPGVcPcVrEnNsRcWVALtPTLAARNas

FIGURE 2B-2

SEQ ID NO:	Isolate	
75	T10	62 vPTTTIRRHVDLLVGAAAFCSAMYVDLGGSVFLVSQVLFVSPRRHET1QDCNCISIYPGH1
62	DK1	62 IPTTTIRRHVDLLVGAAAFCSAMYVDLGGSVFLVSQVLFVSPRRHETaQDCNCISIYPGHV
64	HK4	62 IPTTTIRRHVDLLVGAAAFCSAMYVDLGGSVFLVSQVLFVSPRRHETVQDCNCISIYPGHV
76	US6	62 VPTTTIRRHVDLLVGAAAFCSAMYVDLGGSVFLVSQVLFVSPRRHETVQDCNCISIYPGHV
68	IND8	62 VPTTTIRRHVDLLVGAAAFCSAMYVDLGGSVFLVSQVLFVSPRRHETVQDCNCISIYPGHV
67	IND5	62 VstTTIRRHVDLLVGAAAFCSAMYVDLGGSVFLVSQVLFVSPRRHETVQDCNCISIYPGHV
73	SW2	62 VPTTTIRRHVDLLVGAAAFCSAMYVDLGGSVFLVSQVLFVSPRRHETVQDCNCISIYPGHV
63	HK3	62 VPTTTIRRHVDLLVGAAAFCSAMYVDLGGSVFLVSQVLFVSPRRHETVQDCNCISIYPGHV
66	HK8	62 VPTTTIRRHVDLLVGAAAFCSAMYVDLGGSVFLVSQVLFVSPRRHETVQDCNCISIYPGHV
61	D3	62 VPTTTIRRHVDLLVGAAAFCSAMYVDLGGSVFLVSQVLFVSPRRHETVQeCNCISIYPGHV
74	T3	62 VPTkTIRRHVDLLVGAAAFCSAMYVDLGGSVFLVSQVLFVSPRRHETVQDCNCISIYPGHV
65	HK5	62 VPTTaIRRHVDLLVGAAAFCSAMYVDLGGSVFLVSQVLFVSPRRHETVQDCNCISIYPGHV
71	S45	62 VPTTTIRRHVDLLVGAAAFCSAMYVDLGGSVFLVSQVLFVSPRRHETVQDCNCISIYPGHV
72	SA10	62 VPTTTIRRHVDLLVGAAAFCSAMYVDLGGSVFLVSQVLFVSPRRHETVQDCNCISIYPGrV
69	P10	62 VPTTAIRRHVDLLVGAAAFCSAMYVDLGGSVLLVSQVLFVSPRRHETVQDCNCISIYPGHV
60	D1	62 VPTTAIRRHVDLLVGAAAFCSAMYVDLGGSVFLVSQVLFVSPRRHETVQeCNCISIYPGHV
70	S9	62 VPTTtIRRHVDLLVGAAAFCSAMYVDLGGSVFLVSQVLFVSPRRHETVQnCNCISIYPGHV
60-76	consensus	vpTttIRRHVDLLVGAAAFCSAMYVDLGGSVFLVSQVLFVSPRRHETVQdCNCISIYPGHV

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Appl. No.: 09/084,691 Atty Docket: NIH240.1CPDV1
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FIGURE 2B-3

SEQ ID NO:	Isolate	
75	T10	123 SGHRMAWDMNNWSPTTALVVSQLLRIPQAVmDMVtGAHWGVLAGLAYYSMAGNWAkVLIV
62	DK1	123 SGHRMAWDMNNWSPTTALVVSQLLRIPQAVvDMVAGAHGVLAGLAYYSMAGNWAkVLIV
64	HK4	123 SGHRMAWDMNNWSPTAALVVSQLLRLPQAVMDMVAGAHGVLAGLAYYSMVGNWAkVLIV
76	US6	123 SGHRMAWDMNNWSPTAALVVSQLLRIPQAVMDMVAGAHGVLAGLAYYSMVGNWAkVLIV
68	IND8	123 SGHRMAWDMNNWSPTAALVVSQLLRIPQAVVDVAGAHGVLILAGLAYYSMVGNWAkVLIV
67	IND5	123 SGHRMAWDMNNWSPTAALVVSQLLRIPQAVVDVAGAHGVLILAGLAYYSMVGNWAkVLIV
73	SW2	123 SGHRMAWDMNNWSPTAALVVSQLLRIPQAVVDVAGAHGVLILAGLAYYSMVGNWAkVLIV
63	HK3	123 SGHRMAWDMNNWSPTAALVVSQLLRIPQAVVDVAGAHGVLILAGLAYYSMVGNWAkVLIV
66	HK8	123 SGHRMAWDMNNWSPTALVVSQLLRIPQAVVDVAGAHGVLILAGLAYYSMVGNWAkVLIV
61	D3	123 TGHRMAWDMNNWSPTAALVVSQLLRIPQAVVDVAGAHGVLILAGLAYYSMVGNWAkVLIV
74	T3	123 TGHRMAWDMNNWSPTTALVVSQLLRIPQAVVDVAGAHGVLILAGLAYYSMVGNWAkVLIV
65	HK5	123 TGHRMAWDMNNWSPTTALVVSQLLRIPQAVVDVAGAHGVLILAGLAYYSMVGNWAkVLIV
71	S45	123 TGHRMAWDMNNWSPTAALVVSQLLRIPQAVVDVAGAHGVLILAGLAYYSMVGNWAkVLIV
72	SA10	123 TGHRMAWDMNNWSPTALVVSQLLRIPQAVVDVAGAHGVLILAGLAYYSMVGNWAkVLIV
69	P10	123 sGHRMAWDMNNWSPTAALVVSQLLRIPQAVVDVAGAHGVLILAGLAYYSMVGNWAkVLIV
60	D1	123 TGHRMAWDMNNWSPTTALVVSQLLRIPQAVMDMVAGAHGVLILAGLAYYSMVGNWAkVLIV
70	S9	123 TGHRMAWDMNNWSPTTALVVSQLLRIPQAVMDMVAGAHGVLILAGLAYYSMVGNWAkVLIV
60-76	consensus	SGHRMAWDMNNWSPTAALVVSQLLRIPQAVvDmVaGAHWGVLILAGLAYYSMVGNWAkVLIV

FIGURE 2B-4

<u>SEQ ID NO:</u>	<u>Isolate</u>	
75	T10	184 mLLFAGVDG
62	DK1	184 1LLFAGVDG
64	HK4	184 mLLFAGVDG
76	US6	184 1LLFAGVDG
68	IND8	184 MLLFAGVDG
67	IND5	184 MLLFAGVDG
73	SW2	184 MLLFAGVDG
63	HK3	184 MLLFAGVDG
66	HK8	184 MLLFAGVDG
61	D3	184 MLLFAGVDG
74	T3	184 1LLFAGVDG
65	HK5	184 MLLFAGVDG
71	S45	184 MLLFAGVDG
72	SA10	184 MLLFAGVDG
69	P10	184 MLLFAGVDG
60	D1	184 MLLFAGVDG
70	S9	184 MLLFAGVDG
60-76	consensus	mLLFAGVDG

FIGURE 2C-1

SEQ ID NO:	Isolate	
77	T2	1 AQVrNTsrgYmVTNDcSNesITWQLQAAVLHVPGcIpcErIGNTSRCWIPvtPNVAVRQPG
78	T4	1 AQVKNttnSYmVTNDcSNdsITWQLQAAVLHVPGcVPCekTGNtSRCWIPvSPNVAVRQPG
79	T9	1 AeVKNtSTSYmVTNDcSNdsITWQLQAAVLHVPGcVPCerVGNsSRCWIPvSPNVAVRQPG
80	US10	1 vqVKNTSTSYmVTNDcSNdsITWQLeAAVLHVPGcVPCekVGNTSRCWIPvSPNVAVRQPG
77-80	consensus	aqVKNTstSYmVTNDcSNdsITWQLqAAVLHVPGcVPCe - vGNTSRCWIPvSPNVAV - - PG
SEQ ID NO:	Isolate	
77	T2	62 ALTQGLRTHIDmVMSATLCSALyVGDLcGGvMLAAQMFIVSPrrHwFVQeCNCsIYPGTI
78	T4	62 ALTQGLRTHIDmVMSATLCSALyVGDLcGGvMLAAQMFIVSPQHhWFVQdCNCsIYPGTI
79	T9	62 ALTQGLRTHIDmVMSATLCSALyVGDLcGGvMLAAQMFIIspQHhWFVQeCNCsIYPGTI
80	US10	62 ALTQGLRTHIDmVMSATLCSALyVGDFcGGmMLAAQMFIVSPrrHhsFVQeCNCsIYPGTI
77-80	consensus	ALTQGLRTHIDmVMSATLCSALyVGDLcGGvMLAAQMFIVSP - hHwFVQeCNCsIYPGTI
SEQ ID NO:	Isolate	
77	T2	123 TGHrMAWdMMMNWSPTaTmILAYaMRVPEVIIdIIGaHwGVMFGLAYFSMQGAWAKVVI
78	T4	123 TGHrMAWdMMMNWSPTaTmILAYaMRVPEVIIdIVSGaHwGVMFGLAYFSMQGAWAKVVI
79	T9	123 TGHrMAWdMMMNWSPTtTmILAYaMRVPEVIIdIISGaHwGVMFGLAYFSMQGAWAKVVI
80	US10	123 TGHrMAWdMMMNWSPTaTlILAYvMRVPEVIIdIISGaHwGVLfGLAYFSMQGAWAKVVI
77-80	consensus	TGHrMAWdMMMNWSPTaTmILAYaMRVPEVIIdIISGaHwGVMfGLAYFSMQGAWAKVVI

FIGURE 2C-2

<u>SEQ ID NO:</u>	<u>Isolate</u>	
77	T2	184 LLLAAGVDA
78	T4	184 LLLAAGVDA
79	T9	184 LLLtAGVDA
80	US10	184 LLLaAGVDA
77-80	consensus	LLLaAGVDA

FIGURE 2D-1

SEQ ID NO:	Isolate	
82	DK11	1 VEVNtSSSYATNDCSNsITWQLTNAVHLPGVPCENDNGTLHCWIQVTPNAVKHG
83	SW3	1 VEVNtSSSYATNDCSNsITWQLTNAVHLPGVPCENDNGTLHCWIQVTPNAVKHG
84	T8	1 VEVNtSfSYATNDCSNsITWQLTNAVHLPGVPCENDNGTLRCWIQVTPNAVKHG
81	DK8	1 VEVNtSSSYATNDCSNsITWQLTNAVHLPGVPCENDNGTLRCWIQVTPNAVKHG
81-84	consensus	VEVRN-SsSYATNDCSNsITWQLTNAVHLPGVPCENDNGTL-CWIQVTPNAVKHG
SEQ ID NO:	Isolate	
82	DK11	62 ALTHNLRAHIDMIVMAATVCSALYVGDVCGAVMIVSQAFIVSPEHhFTQECNCsIYQGH
83	SW3	62 ALTHNLRAHIDMIVMAATVCSALYVGDMCGAVMIVSQAFIISPERHNFTQECNCsIYQGR
84	T8	62 ALTHNLRTHVDVIVMAATVCSALYVGDVCGAVMIaSQAFIISPERHNFTQECNCsIYQGH
81	DK8	62 ALTHNLRTHVDVIVMAATVCSALYVGDVCGAVMIVSQALIISPERHNFTQECNCsIYQGH
81-84	consensus	ALTHNLR-HvD-IVMAATVCSALYVGDVCGAVMIVSQAFIISPERHnFTQECNCsIYQGH
SEQ ID NO:	Isolate	
82	DK11	123 TGHrMAWDMMLNWSPTLTMLAYAAARVPPELVLEVFGGHGwVFGLAYFSMQGAWAKVIAI
83	SW3	123 TGHrMAWDMMLNWSPTLTMLAYAAARVPPELVLEVFGGHGwVFGLAYFSMQGAWAKVIAI
84	T8	123 TGHrMAWDMMLNWSPTLTMLAYAAARVPPELVLEVFGGHGwVFGLAYFSMQGAWAKVIAI
81	DK8	123 TGHrMAWDMMLNWSPTLTMLAYAAARVPPELaLqVVFGGHwVFGLAYFSMQGAWAKVIAI
81-84	consensus	TGHrMAWDMMLNWSPTLTMLAYAAARVPPELVLeVVFGGHwVFGLAYFSMQGAWAKVIAI

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Appl. No.: 09/084,691 Atty Docket: NIH240.1CPDV1
REPLACEMENT SHEET

FIGURE 2D-2

<u>SEQ ID NO:</u>	<u>Isolate</u>	
82	DK11	184 LLLVAGVDA
83	SW3	184 LLLVAGVDA
84	T8	184 LLLVAGVDA
81	DK8	184 LLLVAGVDA
81-84	consensus	LLL VAGVDA

FIGURE 2E-1

SEQ ID NO:	Isolate	
86	DK12	1 LEWRNVSGLYVLTNDCsNSSIIVEADDVILHTPGCVPCVQDGNSTCWTSTVTPTVAVRYVG
87	HK10	1 LEWRNVSGLYVLTNDCpNSSIIVEADDVILHTPGCVPCVQDGNSTCWTSTVTPTVAVRYVG
88	S2	1 LEWRNTSGLYVLTNDCSNSSIIVEADDVILHTPGCVPCVQDGNSTCWTPTPTVAVRYVG
90	S54	1 LEWRNTSGLYiLTNDCSNSSIIVEADDVILHTPGCVPCVQDGNSTCWTPTPTVAVRYVG
89	S52	1 LEWRNTSGLYVLTNDCSNSSIIVEADDVILHTPGCVPCVQDGNSTsmCWTPTPTVAVRYVG
86-90	consensus	LEWRNtSGLYvLTNDCsNSSIIVEADDVILHTPGCVPCVQDGNSTtCWTPtVTPTVAVRYVG
86	DK12	62 ATTASIRSHVDLLVGAATMCSALYVGdVCGAVFLVGQAFTFRPRRHQTVQTCNCSLYPGHL
87	HK10	62 ATTASIRSHVDLLVGAATMCSALYVGDMCGAVFLVGQAFTFRPRRHQTVQTCNCSLYPGHL
88	S2	62 ATTASIRSHVDLLVGAATMCSALYVGDMCGAVFLVGQAFTFRPRRHQTVQTCNCSLYPGHL
90	S54	62 ATTASIRSHVDLLVGAATLCSALYVGDMCGAVFLVGQAFTFRPRRHQTVQTCNCSLYPGHL
89	S52	62 ATTASIRSHVDLLVGAATLCSALYVGDMCGAVFLVGQAFTFRPRRHQTVQTCNCSLYPGHv
86-90	consensus	ATTASIRSHVDLLVGAATmCSALYVGDMcGAVFLVGQAFTFRPRRHQTVQTCNCSLYPGHL

FIGURE 2E-2

SEQ ID NO:	Isolate	
86	DK12	123 SGHRMAWDMMNWSPAVGMVVAHVLRLPQTLFDIIAGAHWGIMAGLAYYSMQGNWAKVAII
87	HK10	123 SGHRMAWDMMNWSPAVGMVVAHVLRLPQTLFDIIAGAHWGILAGLAYYSMQGNWAKVAII
88	S2	123 SGHRMAWDMMNWSPAVGMVVAHVLRLPQTVFDIIAGAHWGILAGLAYYSMQGNWAKVAII
90	S54	123 SGHRMAWDMMNWSPAVGMVVAHVLRLPQTLFDIIAGAHWGILAGLAYYSMQGNWAKVAII
89	S52	123 SGHRMAWDMMNWSPAVGMVVAHVLRLPQTLFDIIAGAHWGILAGLAYYSMQGNWAKVAIV
86-90	consensus	SGHRMAWDMMNWSPAVGMVVAHVLRLPQTLFDIIAGAHWGILAGLAYYSMQGNWAKVAII
86	DK12	184 MVMFSGVDA
87	HK10	184 MVMFSGVDA
88	S2	184 MVMFSGVDA
90	S54	184 MIMFSGVDA
89	S52	184 MIMFSGVDA
86-90	consensus	MVMFSGVDA

[illegible]

FIGURE 2G-1

SEQ ID NO:	Isolate	
98	SA5	1 VPYRNASGVVHVTNDPCPNSSIVYEADNLIILHAPGCVPCVkegNVSRCWVQITPTLSAPNLG
100	SA7	1 VPYRNASGVVHVTNDPCPNSSIVYEADNLIILHAPGCVPCVRQnNVSRCWVQITPTLSAPNLG
97	SA4	1 VPYRNASGVVHVTNDPCPNSSIVYEADNLIILHAPGCVPCVRQDNVskCWVQITPTLSAPNLG
96	SA1	1 VPYRNASGVVHVTNDPCPNSSIVYEADsLIILHAPGCVPCVRQDNVSRWVQITPTLSAPtfg
99	SA6	1 VPYRNASGVVHVTNDPCPNSSIVYEADDLIILHAPGCVPCVRkDNVSRWVhITPTLSAPSLG
101	SA13	1 VPYRNASGVVHVTNDPCPNSSIVYEADDLIILHAPGCVPCVRgqNVSRCWVqITPTLSAPSLG
96-101	consensus	VPYRNASGVVHVTNDPCPNSSIVYEADnLIILHAPGCVPCVrqdNVSrCWVqITPTLSAPnlg
98	SA5	62 AVTAPLRRvVDYLAGGAALCSALYVGDA CGAVFLVGQMFtYRPRQHTTVQDCNCsIYSGHI
100	SA7	62 AVTAPLRRvVDYLAGGAALCSALYVGDA CGAVFLVGQMFsYRPRQHTTVQDCNCsIYSGHI
97	SA4	62 AVTAPLRRvVDYLAGGAALCSALYVGDA CGAVFLVGQMFtYRPRQHTTVQDCNCsIYSGHI
96	SA1	62 AVTAPLRRvVDYLAGGAALCSALYVGDA CGAVFLVGQMFtYRPRQHTTVQDCNCsIYSGHI
99	SA6	62 AVTAPLRRvVDYLAGGAALCSALYVGDV CGALFLVGQMFtYRPRQHaTVQDCNCsIYSGHI
101	SA13	62 AVTAPLRRvVDYLAGGAALCSALYVGDA CGAVFLVGQMFtYsPRrHnvVQDCNCsIYSGHI
96-101	consensus	AVTAPLRRvVDYLAGGAALCSALYVGDA CGAVFLVGQMFtYrPRqHttVQDCNCsIYSGHI

FIGURE 2G-2

SEQ ID NO:	Isolate	
98	SA5	123 TGHMAWDMMNWSPPTTALVMAQVLRIPQVWIDIIAGGHWGVLFAVAYFASAANWAKVVLV
100	SA7	123 TGHMAWDMMNWSPPTTALVMAQVLRIPQVWIDIIAGGHWGVLFAVAYFASAANWAKVVLV
97	SA4	123 TGHMAWDMMNWSPPTTALLMAQLLRIPQVWIDIIAGGHWGVLFAVAYFASAANWAKVVLV
96	SA1	123 TGHMAWDMMNWSPPTTALLMAQMLRIPQVWIDIIAGGHWGVLFAVAYFASAANWAKVVLV
99	SA6	123 TGHMAWDMMNWSPaTALVMAQMLRIPQVWIDIIAGGHWGVLFAVAYFASAANWAKVVLV
101	SA13	123 TGHMAWDMMNWSPcTALVMAQLLRIPQVWIDIIAGaHWGVLFAAAAYASAANWAKVVLV
96-101	consensus	TGHMAWDMMNWSPcTALVMAQLLRIPQVWIDIIAGgHWGVLFAaAYFASAANWAKVVLV
98	Isolate SA5	184 LFLFAGVDg
100	SA7	184 LFLFAGVDA
97	SA4	184 LFLFAGVDA
96	SA1	184 LFLFAGVDg
99	SA6	184 LFLFAGVDA
101	SA13	184 LFLFAGVDA
96-101	consensus	LFLFAGVDA

SEQ ID NO:	Genotype	consensus
81-84	(IV/2b)	
85	(2c)	
77-80	(III/2a)	
86-90	(V/3a)	
60-76	(II/1b)	
52-59	(I/1a)	
91	(4a)	
93-94	(4c)	
95	(4d)	
92	(4b)	
96-101	(5a)	
102	(6a)	
52-102	consensus	

SEQ ID NO:	Genotype	consensus
81-84	(IV/2b)	
85	(2c)	
77-80	(III/2a)	
86-90	(V/3a)	
60-76	(II/1b)	
52-59	(I/1a)	
91	(4a)	
93-94	(4c)	
95	(4d)	
92	(4b)	
96-101	(5a)	
102	(6a)	
52-102	consensus	

SEQ ID NO:	Genotype	consensus
81-84	(IV/2b)	
85	(2c)	
77-80	(III/2a)	
86-90	(V/3a)	
60-76	(II/1b)	
52-59	(I/1a)	
91	(4a)	
93-94	(4c)	
95	(4d)	
92	(4b)	
96-101	(5a)	
102	(6a)	
52-102	consensus	

SEQ ID NO:	Genotype	consensus
81-84	(IV/2b)	
85	(2c)	
77-80	(III/2a)	
86-90	(V/3a)	
60-76	(II/1b)	
52-59	(I/1a)	
91	(4a)	
93-94	(4c)	
95	(4d)	
92	(4b)	
96-101	(5a)	
102	(6a)	
52-102	consensus	

SEQ ID NO:	Genotype	consensus
81-84	(IV/2b)	
85	(2c)	
77-80	(III/2a)	
86-90	(V/3a)	
60-76	(II/1b)	
52-59	(I/1a)	
91	(4a)	
93-94	(4c)	
95	(4d)	
92	(4b)	
96-101	(5a)	
102	(6a)	
52-102	consensus	

SEQ ID NO:	Genotype	consensus
81-84	(IV/2b)	
85	(2c)	
77-80	(III/2a)	
86-90	(V/3a)	
60-76	(II/1b)	
52-59	(I/1a)	
91	(4a)	
93-94	(4c)	
95	(4d)	
92	(4b)	
96-101	(5a)	
102	(6a)	
52-102	consensus	

SEQ ID NO:	Genotype	consensus
81-84	(IV/2b)	
85	(2c)	
77-80	(III/2a)	
86-90	(V/3a)	
60-76	(II/1b)	
52-59	(I/1a)	
91	(4a)	
93-94	(4c)	
95	(4d)	
92	(4b)	
96-101	(5a)	
102	(6a)	
52-102	consensus	

SEQ ID NO:	Genotype	consensus
81-84	(IV/2b)	
85	(2c)	
77-80	(III/2a)	
86-90	(V/3a)	
60-76	(II/1b)	
52-59	(I/1a)	
91	(4a)	
93-94	(4c)	
95	(4d)	
92	(4b)	
96-101	(5a)	
102	(6a)	
52-102	consensus	

SEQ ID NO:	Genotype	consensus
81-84	(IV/2b)	
85	(2c)	
77-80	(III/2a)	
86-90	(V/3a)	
60-76	(II/1b)	
52-59	(I/1a)	
91	(4a)	
93-94	(4c)	
95	(4d)	
92	(4b)	
96-101	(5a)	
102	(6a)	
52-102	consensus	

SEQ ID NO:	Genotype	consensus
81-84	(IV/2b)	
85	(2c)	
77-80	(III/2a)	
86-90	(V/3a)	
60-76	(II/1b)	
52-59	(I/1a)	
91	(4a)	
93-94	(4c)	
95	(4d)	
92	(4b)	
96-101	(5a)	
102	(6a)	
52-102	consensus	

SEQ ID NO:	Genotype	consensus
81-84		

FIGURE 3A

Genotype	SEQ ID NO: 52-102	Isolate	yevrnsgv hvtndcs nss iweaada l htpgcvpcvregntsr ckhavtptvaarnagapt ttr hrvollvgaa tcsa lrvvgd lbgsvflv	200	210	220	230	240	250	260	270	280
IV/2b	82	DK11	VEVRN TSS- YA	---	S- n- ITWLTNAVL- L	---	V- EMDNGTLH- -	---	[QVT- NVAVIRGAL THRL- AH- MIWMA- TV- AL- V- V- AVNIV			
	83	SU3	VEVRN TSS- YA	---	S- s- ITWLTNAVL- L	---	V- EMDNGTLH- -	---	[QVT- NVAVIRGAL THRL- ANV- MIWMA- TV- AL- V- V- AVNIV			
	81	DK8	VEVRN TSS- YA	---	S- N- ITWLTNAVL- L	---	V- EMDNGTLH- -	---	[QVT- NVAVIRGAL THRL- THV- VIWMA- TV- AL- V- V- AVNIV			
	84	T8	VEVRN TSS- YA	---	S- N- ITWLTNAVL- L	---	V- EMDNGTLH- -	---	[QVT- NVAVIRGAL THRL- THV- VIWMA- TV- AL- V- V- AVNIV			
	85	S83	VEVRN TSS- YA	---	S- s- ITWLTNAVL- L	---	V- EMDNGTLH- -	---	[QVT- NVAVIRGAL THRL- THV- VIWMA- TV- AL- V- V- AVNIV			
II1/2a	86	US10	VEVRN TSS- YA	---	S- D- ITWLTNAVL- L	---	V- EMDNGTLH- -	---	[QVT- NVAVIRGAL THRL- THV- VIWMA- TV- AL- V- V- AVNIV			
	87	T9	VEVRN TSS- YA	---	S- D- ITWLTNAVL- L	---	V- EMDNGTLH- -	---	[QVT- NVAVIRGAL THRL- THV- VIWMA- TV- AL- V- V- AVNIV			
	88	T2	VEVRN TSS- YA	---	S- D- ITWLTNAVL- L	---	V- EMDNGTLH- -	---	[QVT- NVAVIRGAL THRL- THV- VIWMA- TV- AL- V- V- AVNIV			
	89	DK12	VEVRN TSS- YA	---	S- D- ITWLTNAVL- L	---	V- EMDNGTLH- -	---	[QVT- NVAVIRGAL THRL- THV- VIWMA- TV- AL- V- V- AVNIV			
	90	HK10	VEVRN TSS- YA	---	S- D- ITWLTNAVL- L	---	V- EMDNGTLH- -	---	[QVT- NVAVIRGAL THRL- THV- VIWMA- TV- AL- V- V- AVNIV			
(V)/3a	91	S54	VEVRN TSS- YA	---	S- S- ITWLTNAVL- L	---	V- EMDNGTLH- -	---	[QVT- NVAVIRGAL THRL- THV- VIWMA- TV- AL- V- V- AVNIV			
	92	S52	VEVRN TSS- YA	---	S- S- ITWLTNAVL- L	---	V- EMDNGTLH- -	---	[QVT- NVAVIRGAL THRL- THV- VIWMA- TV- AL- V- V- AVNIV			
	93	IND8	VEVRN TSS- YA	---	S- S- ITWLTNAVL- L	---	V- EMDNGTLH- -	---	[QVT- NVAVIRGAL THRL- THV- VIWMA- TV- AL- V- V- AVNIV			
	94	IND5	VEVRN TSS- YA	---	S- S- ITWLTNAVL- L	---	V- EMDNGTLH- -	---	[QVT- NVAVIRGAL THRL- THV- VIWMA- TV- AL- V- V- AVNIV			
	95	SM2	VEVRN TSS- YA	---	S- S- ITWLTNAVL- L	---	V- EMDNGTLH- -	---	[QVT- NVAVIRGAL THRL- THV- VIWMA- TV- AL- V- V- AVNIV			
II1/b	96	HK3	VEVRN TSS- YA	---	S- S- ITWLTNAVL- L	---	V- EMDNGTLH- -	---	[QVT- NVAVIRGAL THRL- THV- VIWMA- TV- AL- V- V- AVNIV			
	97	HK3	VEVRN TSS- YA	---	S- S- ITWLTNAVL- L	---	V- EMDNGTLH- -	---	[QVT- NVAVIRGAL THRL- THV- VIWMA- TV- AL- V- V- AVNIV			
	98	S45	VEVRN TSS- YA	---	S- S- ITWLTNAVL- L	---	V- EMDNGTLH- -	---	[QVT- NVAVIRGAL THRL- THV- VIWMA- TV- AL- V- V- AVNIV			
	99	D3	VEVRN TSS- YA	---	S- S- ITWLTNAVL- L	---	V- EMDNGTLH- -	---	[QVT- NVAVIRGAL THRL- THV- VIWMA- TV- AL- V- V- AVNIV			
	100	T3	VEVRN TSS- YA	---	S- S- ITWLTNAVL- L	---	V- EMDNGTLH- -	---	[QVT- NVAVIRGAL THRL- THV- VIWMA- TV- AL- V- V- AVNIV			
I/1a	101	HK5	VEVRN TSS- YA	---	S- S- ITWLTNAVL- L	---	V- EMDNGTLH- -	---	[QVT- NVAVIRGAL THRL- THV- VIWMA- TV- AL- V- V- AVNIV			
	102	HK4	VEVRN TSS- YA	---	S- S- ITWLTNAVL- L	---	V- EMDNGTLH- -	---	[QVT- NVAVIRGAL THRL- THV- VIWMA- TV- AL- V- V- AVNIV			
	103	US6	VEVRN TSS- YA	---	S- S- ITWLTNAVL- L	---	V- EMDNGTLH- -	---	[QVT- NVAVIRGAL THRL- THV- VIWMA- TV- AL- V- V- AVNIV			
	104	P10	VEVRN TSS- YA	---	S- S- ITWLTNAVL- L	---	V- EMDNGTLH- -	---	[QVT- NVAVIRGAL THRL- THV- VIWMA- TV- AL- V- V- AVNIV			
	105	SA10	VEVRN TSS- YA	---	S- S- ITWLTNAVL- L	---	V- EMDNGTLH- -	---	[QVT- NVAVIRGAL THRL- THV- VIWMA- TV- AL- V- V- AVNIV			
4a	106	DK1	VEVRN TSS- YA	---	S- S- ITWLTNAVL- L	---	V- EMDNGTLH- -	---	[QVT- NVAVIRGAL THRL- THV- VIWMA- TV- AL- V- V- AVNIV			
	107	S9	VEVRN TSS- YA	---	S- S- ITWLTNAVL- L	---	V- EMDNGTLH- -	---	[QVT- NVAVIRGAL THRL- THV- VIWMA- TV- AL- V- V- AVNIV			
	108	D1	VEVRN TSS- YA	---	S- S- ITWLTNAVL- L	---	V- EMDNGTLH- -	---	[QVT- NVAVIRGAL THRL- THV- VIWMA- TV- AL- V- V- AVNIV			
	109	DK7	VEVRN TSS- YA	---	S- S- ITWLTNAVL- L	---	V- EMDNGTLH- -	---	[QVT- NVAVIRGAL THRL- THV- VIWMA- TV- AL- V- V- AVNIV			
	110	US11	VEVRN TSS- YA	---	S- S- ITWLTNAVL- L	---	V- EMDNGTLH- -	---	[QVT- NVAVIRGAL THRL- THV- VIWMA- TV- AL- V- V- AVNIV			
4c	111	DR4	VEVRN TSS- YA	---	S- S- ITWLTNAVL- L	---	V- EMDNGTLH- -	---	[QVT- NVAVIRGAL THRL- THV- VIWMA- TV- AL- V- V- AVNIV			
	112	DR1	VEVRN TSS- YA	---	S- S- ITWLTNAVL- L	---	V- EMDNGTLH- -	---	[QVT- NVAVIRGAL THRL- THV- VIWMA- TV- AL- V- V- AVNIV			
	113	DK9	VEVRN TSS- YA	---	S- S- ITWLTNAVL- L	---	V- EMDNGTLH- -	---	[QVT- NVAVIRGAL THRL- THV- VIWMA- TV- AL- V- V- AVNIV			
	114	SW1	VEVRN TSS- YA	---	S- S- ITWLTNAVL- L	---	V- EMDNGTLH- -	---	[QVT- NVAVIRGAL THRL- THV- VIWMA- TV- AL- V- V- AVNIV			
	115	S14	VEVRN TSS- YA	---	S- S- ITWLTNAVL- L	---	V- EMDNGTLH- -	---	[QVT- NVAVIRGAL THRL- THV- VIWMA- TV- AL- V- V- AVNIV			
5a	116	S18	VEVRN TSS- YA	---	S- S- ITWLTNAVL- L	---	V- EMDNGTLH- -	---	[QVT- NVAVIRGAL THRL- THV- VIWMA- TV- AL- V- V- AVNIV			
	117	Z4	VEVRN TSS- YA	---	S- S- ITWLTNAVL- L	---	V- EMDNGTLH- -	---	[QVT- NVAVIRGAL THRL- THV- VIWMA- TV- AL- V- V- AVNIV			
	118	Z6	VEVRN TSS- YA	---	S- S- ITWLTNAVL- L	---	V- EMDNGTLH- -	---	[QVT- NVAVIRGAL THRL- THV- VIWMA- TV- AL- V- V- AVNIV			
	119	Z7	VEVRN TSS- YA	---	S- S- ITWLTNAVL- L	---	V- EMDNGTLH- -	---	[QVT- NVAVIRGAL THRL- THV- VIWMA- TV- AL- V- V- AVNIV			
	120	DK13	VEVRN TSS- YA	---	S- S- ITWLTNAVL- L	---	V- EMDNGTLH- -	---	[QVT- NVAVIRGAL THRL- THV- VIWMA- TV- AL- V- V- AVNIV			
6a	121	Z1	VEVRN TSS- YA	---	S- S- ITWLTNAVL- L	---	V- EMDNGTLH- -	---	[QVT- NVAVIRGAL THRL- THV- VIWMA- TV- AL- V- V- AVNIV			
	122	SA5	VEVRN TSS- YA	---	S- S- ITWLTNAVL- L	---	V- EMDNGTLH- -	---	[QVT- NVAVIRGAL THRL- THV- VIWMA- TV- AL- V- V- AVNIV			
	123	SA7	VEVRN TSS- YA	---	S- S- ITWLTNAVL- L	---	V- EMDNGTLH- -	---	[QVT- NVAVIRGAL THRL- THV- VIWMA- TV- AL- V- V- AVNIV			
	124	SA4	VEVRN TSS- YA	---	S- S- ITWLTNAVL- L	---	V- EMDNGTLH- -	---	[QVT- NVAVIRGAL THRL- THV- VIWMA- TV- AL- V- V- AVNIV			
	125	SA1	VEVRN TSS- YA	---	S- S- ITWLTNAVL- L	---	V- EMDNGTLH- -	---	[QVT- NVAVIRGAL THRL- THV- VIWMA- TV- AL- V- V- AVNIV			

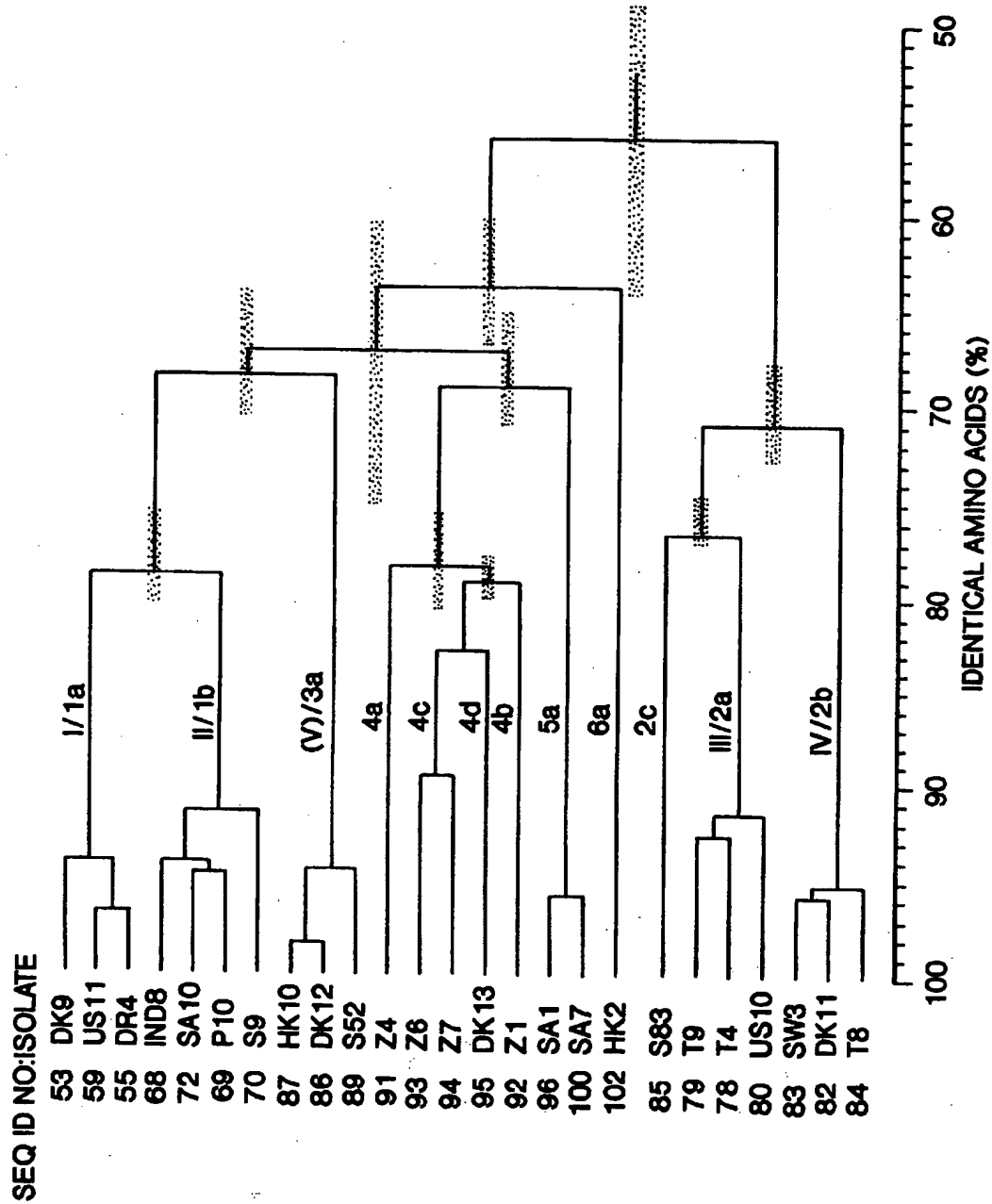
FIGURE 3B

Genotype	SEQ ID NO:	Isolate	290	300	310	320	330	340	350	360	370	380
1V/2b	82	DK11	S-AFVS-ErhFT-E	I-Q-HIT	L-TLNLAYAA-V-ELVLEWF-G	VFGL-YFSHGA-A	IAILLVA--DA					
	83	SV3	S-AFVS-ErhFT-E	I-Q-HIT	L-TLNLAYAA-V-ELVLEWF-G	VFGL-YFSHGA-A	IAILLVA--DA					
	81	DK3	S-AFVS-ErhFT-E	I-Q-HIT	L-TLNLAYAA-V-ELVLEWF-G	VFGL-YFSHGA-A	IAILLVA--DA					
	84	T8	S-AFVS-ErhFT-E	I-Q-HIT	L-TLNLAYAA-V-ELVLEWF-G	VFGL-YFSHGA-A	IAILLVA--DA					
	85	SV3	S-AFVS-ErhFT-E	I-Q-HIT	L-TLNLAYAA-V-ELVLEWF-G	VFGL-YFSHGA-A	IAILLVA--DA					
111/2a	78	US10	A-MFVS-QHNFV-E	I-P-TIT	M-TLNLAYAA-V-EVIDIIS-A	VFGL-YFSHGA-A	IAILLVA--DA					
	80	T9	A-MFVS-QHNFV-E	I-P-TIT	M-TLNLAYAA-V-EVIDIIS-A	VFGL-YFSHGA-A	IAILLVA--DA					
	79	T9	A-MFVS-QHNFV-E	I-P-TIT	M-TLNLAYAA-V-EVIDIIS-A	VFGL-YFSHGA-A	IAILLVA--DA					
	77	T2	A-MFVS-QHNFV-E	I-P-TIT	M-TLNLAYAA-V-EVIDIIS-A	VFGL-YFSHGA-A	IAILLVA--DA					
	86	DK12	G-AFTER-RRHQT-V	I-P-HVS	M-AVGNVAVL-L-QTLFDIA-A	ILAGL-YFSHGA-A	IAILLVA--DA					
(V)/3a	87	HK10	G-AFTER-RRHQT-V	I-P-HVS	M-AVGNVAVL-L-QTLFDIA-A	ILAGL-YFSHGA-A	IAILLVA--DA					
	88	S2	G-AFTER-RRHQT-V	I-P-HVS	M-AVGNVAVL-L-QTLFDIA-A	ILAGL-YFSHGA-A	IAILLVA--DA					
	90	S54	G-AFTER-RRHQT-V	I-P-HVS	M-AVGNVAVL-L-QTLFDIA-A	ILAGL-YFSHGA-A	IAILLVA--DA					
	89	S52	G-AFTER-RRHQT-V	I-P-HVS	M-AVGNVAVL-L-QTLFDIA-A	ILAGL-YFSHGA-A	IAILLVA--DA					
	68	IND8	S-LFTFS-RRHETV-D	I-P-HVS	M-TALVWSQLL-I-QAVDHA-A	VLGL-YFSHGA-A	IAILLVA--DA					
11/1b	67	IND5	S-LFTFS-RRHETV-D	I-P-HVS	M-TALVWSQLL-I-QAVDHA-A	VLGL-YFSHGA-A	IAILLVA--DA					
	73	SH2	S-LFTFS-RRHETV-D	I-P-HVS	M-TALVWSQLL-I-QAVDHA-A	VLGL-YFSHGA-A	IAILLVA--DA					
	63	HK3	S-LFTFS-RRHETV-D	I-P-HVS	M-TALVWSQLL-I-QAVDHA-A	VLGL-YFSHGA-A	IAILLVA--DA					
	66	HK8	S-LFTFS-RRHETV-D	I-P-HVS	M-TALVWSQLL-I-QAVDHA-A	VLGL-YFSHGA-A	IAILLVA--DA					
	71	SA5	S-LFTFS-RRHETV-D	I-P-HVS	M-TALVWSQLL-I-QAVDHA-A	VLGL-YFSHGA-A	IAILLVA--DA					
1/1a	61	D3	S-LFTFS-RRHETV-D	I-P-HVS	M-TALVWSQLL-I-QAVDHA-A	VLGL-YFSHGA-A	IAILLVA--DA					
	74	T3	S-LFTFS-RRHETV-D	I-P-HVS	M-TALVWSQLL-I-QAVDHA-A	VLGL-YFSHGA-A	IAILLVA--DA					
	65	HK5	S-LFTFS-RRHETV-D	I-P-HVS	M-TALVWSQLL-I-QAVDHA-A	VLGL-YFSHGA-A	IAILLVA--DA					
	64	HK4	S-LFTFS-RRHETV-D	I-P-HVS	M-TALVWSQLL-I-QAVDHA-A	VLGL-YFSHGA-A	IAILLVA--DA					
	76	US6	S-LFTFS-RRHETV-D	I-P-HVS	M-TALVWSQLL-I-QAVDHA-A	VLGL-YFSHGA-A	IAILLVA--DA					
1/1a	69	P10	S-LFTFS-RRHETV-D	I-P-HVS	M-TALVWSQLL-I-QAVDHA-A	VLGL-YFSHGA-A	IAILLVA--DA					
	72	SA10	S-LFTFS-RRHETV-D	I-P-HVS	M-TALVWSQLL-I-QAVDHA-A	VLGL-YFSHGA-A	IAILLVA--DA					
	75	T10	S-LFTFS-RRHETV-D	I-P-HVS	M-TALVWSQLL-I-QAVDHA-A	VLGL-YFSHGA-A	IAILLVA--DA					
	62	DK1	S-LFTFS-RRHETV-D	I-P-HVS	M-TALVWSQLL-I-QAVDHA-A	VLGL-YFSHGA-A	IAILLVA--DA					
	70	S9	S-LFTFS-RRHETV-D	I-P-HVS	M-TALVWSQLL-I-QAVDHA-A	VLGL-YFSHGA-A	IAILLVA--DA					
1/1a	60	D1	S-LFTFS-RRHETV-D	I-P-HVS	M-TALVWSQLL-I-QAVDHA-A	VLGL-YFSHGA-A	IAILLVA--DA					
	52	DK7	G-LFTFS-RRHETV-D	I-P-HIT	M-TALVWSQLL-I-QAVDHA-A	VLGL-YFSHGA-A	IAILLVA--DA					
	59	US11	G-LFTFS-RRHETV-D	I-P-HIT	M-TALVWSQLL-I-QAVDHA-A	VLGL-YFSHGA-A	IAILLVA--DA					
	55	DR4	G-LFTFS-RRHETV-D	I-P-HIT	M-TALVWSQLL-I-QAVDHA-A	VLGL-YFSHGA-A	IAILLVA--DA					
	54	DR1	G-LFTFS-RRHETV-D	I-P-HIT	M-TALVWSQLL-I-QAVDHA-A	VLGL-YFSHGA-A	IAILLVA--DA					
1/1a	53	DK9	G-LFTFS-RRHETV-D	I-P-HIT	M-TALVWSQLL-I-QAVDHA-A	VLGL-YFSHGA-A	IAILLVA--DA					
	58	SA1	G-LFTFS-RRHETV-D	I-P-HIT	M-TALVWSQLL-I-QAVDHA-A	VLGL-YFSHGA-A	IAILLVA--DA					
	56	SA14	G-LFTFS-RRHETV-D	I-P-HIT	M-TALVWSQLL-I-QAVDHA-A	VLGL-YFSHGA-A	IAILLVA--DA					
	57	SA18	G-LFTFS-RRHETV-D	I-P-HIT	M-TALVWSQLL-I-QAVDHA-A	VLGL-YFSHGA-A	IAILLVA--DA					
	91	Z4	G-LFTFS-RRHETV-D	I-P-HIT	M-TALVWSQLL-I-QAVDHA-A	VLGL-YFSHGA-A	IAILLVA--DA					
1/1a	93	Z6	G-LFTFS-RRHETV-D	I-P-HIT	M-TALVWSQLL-I-QAVDHA-A	VLGL-YFSHGA-A	IAILLVA--DA					
	94	Z7	G-LFTFS-RRHETV-D	I-P-HIT	M-TALVWSQLL-I-QAVDHA-A	VLGL-YFSHGA-A	IAILLVA--DA					
	95	DK13	G-LFTFS-RRHETV-D	I-P-HIT	M-TALVWSQLL-I-QAVDHA-A	VLGL-YFSHGA-A	IAILLVA--DA					
	92	Z1	G-LFTFS-RRHETV-D	I-P-HIT	M-TALVWSQLL-I-QAVDHA-A	VLGL-YFSHGA-A	IAILLVA--DA					
	98	SA5	G-LFTFS-RRHETV-D	I-P-HIT	M-TALVWSQLL-I-QAVDHA-A	VLGL-YFSHGA-A	IAILLVA--DA					
1/1a	100	SA7	G-LFTFS-RRHETV-D	I-P-HIT	M-TALVWSQLL-I-QAVDHA-A	VLGL-YFSHGA-A	IAILLVA--DA					
	97	SA4	G-LFTFS-RRHETV-D	I-P-HIT	M-TALVWSQLL-I-QAVDHA-A	VLGL-YFSHGA-A	IAILLVA--DA					
	96	SA1	G-LFTFS-RRHETV-D	I-P-HIT	M-TALVWSQLL-I-QAVDHA-A	VLGL-YFSHGA-A	IAILLVA--DA					
	99	SA6	G-LFTFS-RRHETV-D	I-P-HIT	M-TALVWSQLL-I-QAVDHA-A	VLGL-YFSHGA-A	IAILLVA--DA					
	101	SA13	G-LFTFS-RRHETV-D	I-P-HIT	M-TALVWSQLL-I-QAVDHA-A	VLGL-YFSHGA-A	IAILLVA--DA					
1/1a	102	HK2	G-LFTFS-RRHETV-D	I-P-HIT	M-TALVWSQLL-I-QAVDHA-A	VLGL-YFSHGA-A	IAILLVA--DA					
			G-LFTFS-RRHETV-D	I-P-HIT	M-TALVWSQLL-I-QAVDHA-A	VLGL-YFSHGA-A	IAILLVA--DA					

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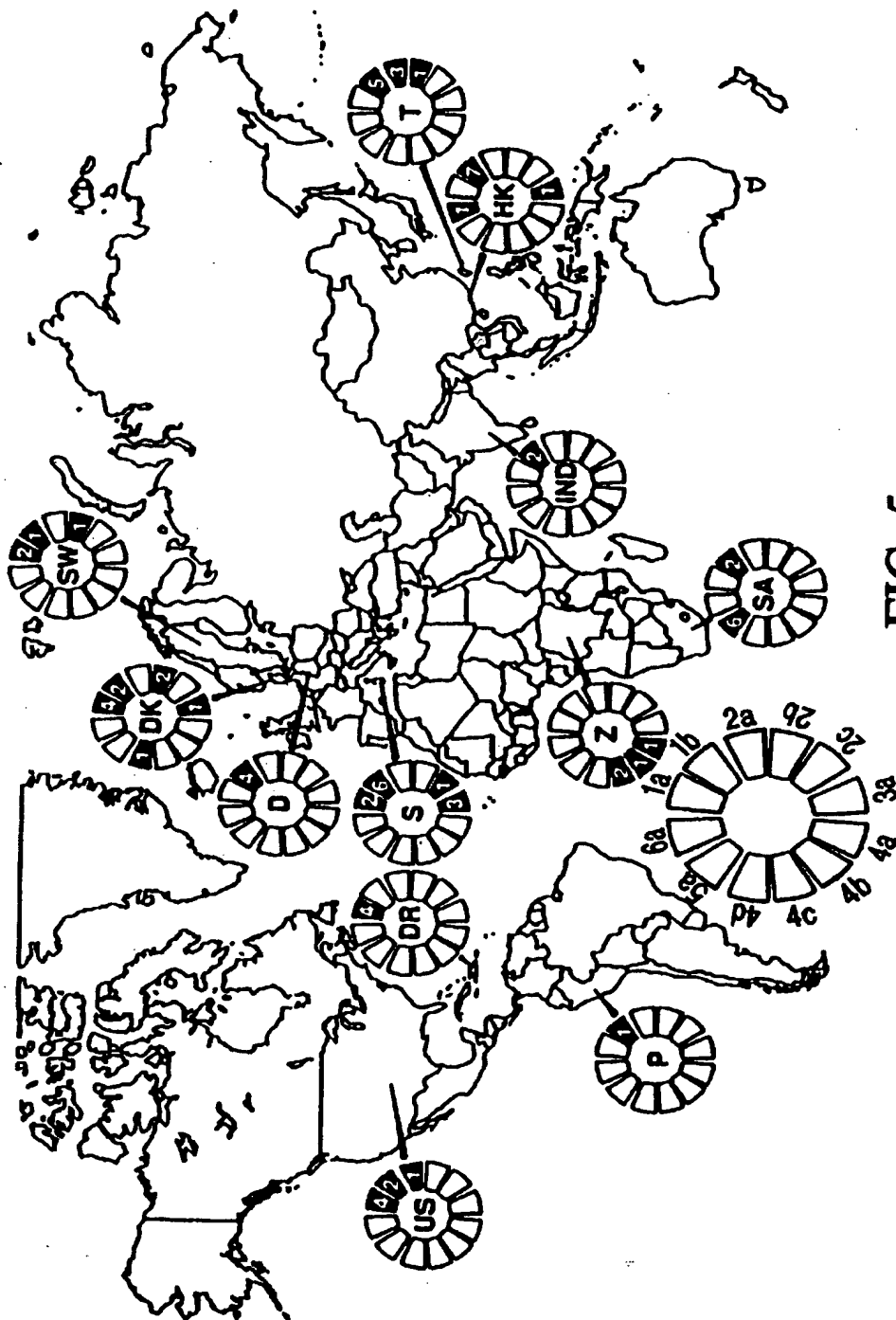


FIGURE 6A-1

SEQ ID NO:	ISOLATE	
108	DR4	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAAACCAACGTAACACCAACCGTCGCCCCACAGG
103	DK7	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAAACCAACGTAACACCAACCGTCGCCCCACAGG
104	US11	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAAACCAACGTAACACCAACCGTCGCCCCACAGG
105	S14	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAAACCAACGTAACACCAACCGTCGCCCCACAGG
106	SW1	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAAACCAACGTAACACCAACCGTCGCCCCACAGG
107	S18	1 ATGAGCACaAATCCTAAACCTCAAAGAAAAAACCAACGTAACACCAACCGTCGCCCCACAGG
103-108	consensus	ATGAGCACgAATCCTAAACCTCAAAGAAAAAACCAACGTAACACCAACCGTCGCCCCACAGG
SEQ ID NO:	ISOLATE	
108	DR4	62 ACGTCAAGTTCCCGGTGGCGGTCAAGTCGTTGGTGGAGTTTACTTGTGCGCGCAGGGG
103	DK7	62 ACGTCAAGTTCCCGGTGGCGGTCAAGTCGTTGGTGGAGTTTACTTGTGCGCGCAGGGG
104	US11	62 ACGTCAAGTTCCCGGTGGCGGTCAAGTCGTTGGTGGAGTTTACTTGTGCGCGCAGGGG
105	S14	62 ACGTCAAGTTCCCGGTGGCGGTCAAGTCGTTGGTGGAGTTTACTTGTGCGCGCAGGGG
106	SW1	62 ACGTCAAGTTCCCGGTGGCGGTCAAGTCGTTGGTGGAGTTTACTTGTGCGCGCAGGGG
107	S18	62 ACGTCAAGTTCCCGGTGGCGGTCAAGTCGTTGGTGGAGTTTACTTGTGCGCGCAGGGG
103-108	consensus	ACGTCAAGTTCCCGGTGGCGGTCAAGTCGTTGGTGGAGTTTACTTGTGCGCGCAGGGG
SEQ ID NO:	ISOLATE	
108	DR4	123 CCCTAGATTGGGTGTGCGCGGcCGAGGAAGACTTCCGAGCGGTCCGAACCTCGAGGTAGA
103	DK7	123 CCCTAGATTGGGTGTGCGCGGcCGAGGAAGACTTCCGAGCGGTCCGAACCTCGAGGTAGA
104	US11	123 CCCTAGATTGGGTGTGCGCGGcCGAGGAAGACTTCCGAGCGGTCCGAACCTCGAGGTAGA
105	S14	123 CCCTAGATTGGGTGTGCGCGGcCGAGGAAGACTTCCGAGCGGTCCGAACCTCGAGGTAGA
106	SW1	123 CCCTAGATTGGGTGTGCGCGGcCGAGGAAGACTTCCGAGCGGTCCGAACCTCGAGGTAGA
107	S18	123 CCCTAGATTGGGTGTGCGCGGcCGAGGAAGACTTCCGAGCGGTCCGAACCTCGAGGTAGA
103-108	consensus	CCCTAGATTGGGTGTGCGCGGcCGAGGAAGACTTCCGAGCGGTCCGAACCTCGAGGTAGA

FIGURE 6A-2

SEQ ID NO:	ISOLATE	
108	DR4	184 CGTCAGCCTATCCCCAAGGCGCGTCGGCCCCAGGGCAGGACCTGGGCTCAGCCCCGGGTACC
103	DK7	184 CGTCAGCCTATCCCCAAGGACGTCGGCCCCAGGGCAGGACCTGGGCTCAGCCCCGGGTACC
104	US11	184 CGTCAGCCTATCCCCAAGGACGTCGGCCCCAGGGCAGGACCTGGGCTCAGCCCCGGGTACC
105	S14	184 CGTCAGCCTATCCCCAAGGACGTCGGCCCCAGGGCAGGACCTGGGCTCAGCCCCGGGTATC
106	SW1	184 CGTCAGCCTATCCCCAAGGCGCGTCGGCCCCAGGGCAGGACCTGGGCTCAGCCCCGGGTATC
107	S18	184 CGTCAGCCTATCCCCAAGGCGCGTCGGCCCCAGGGCAGGACCTGGGCTCAGCCCCGGGTACC
103-108	consensus	CGTCAGCCTATCCCCAAGGC - CGTCGGCCCCAGGGCAGGACCTGGGCTCAGCCCCGGGTACC
SEQ ID NO:	ISOLATE	
108	DR4	245 CTTGGCCCCCTCTATGGCAATGAGGGCTGCGGGTGGGCGGGATGGCTCCTGTCCCCCGTGG
103	DK7	245 CTTGGCCCCCTCTATGGCAATGAGGGCTGCGGGTGGGCGGGATGGCTCCTGTCCCCCGTGG
104	US11	245 CTTGGCCCCCTCTATGGCAATGAGGGCTGCGGGTGGGCGGGATGGCTCCTGTCCCCCGTGG
105	S14	245 CTTGGCCCCCTCTATGGCAATGAGGGCTGCGGGTGGGCGGGATGGCTCCTGTCCCCCGTGG
106	SW1	245 CTTGGCCCCCTCTATGGCAATGAGGGCTGCGGaTGGGCGGGATGGCTCCTGTCCCCCGTGG
107	S18	245 CTTGGCCCCCTCTATGGCAATGAGGGCTGCGGgTGGGCGGGATGGCTCCTGTCCCCCGTGG
103-108	consensus	CTTGGCCCCCTCTATGGCAATGAGGGCTGCGGgTGGGCGGGATGGCTCCTGTCC - CCCCCTGG
SEQ ID NO:	ISOLATE	
108	DR4	306 CTCTCGGCCCTAGCTGGGGCCCCACAGACCCCGGCGtAGGTCCGCAATTTGGGTAAGGTC
103	DK7	306 CTCTCGGCCCTAGCTGGGGCCCCACAGACCCCGGCGcAGGTCCGCAATTTGGGTAAGGTC
104	US11	306 CTCTCGGCCCTAGCTGGGGCCCCACgGACCCCGGCGTAGGTCCGCAATTTGGGTAAGGTC
105	S14	306 CTCTCGGCCCTAGCTGGGGCCCCACAGACCCCGGCGTAGGTCCGCAATTTGGGTAAGGTC
106	SW1	306 CTCTCGGCCCTAGCTGGGGCCCCACAGACCCCGGCGTAGGTCCGCAATTTGGGTAAGGTC
107	S18	306 CTCcCGGCCCTAGCTGGGGCCCCACAGACCCCGGCGTAGGTCCGCAATTTGGGcAAAGTC
103-108	consensus	CTCtCGGCCCTAGCTGGGGCCCCcAcAGACCCCGGCGtAGGTCCGCAATTTGGGtAAGGTC

FIGURE 6A-3

SEQ ID NO:	ISOLATE	
108	DR4	367 ATCGAACCCCTcACGTGCGGCTTCGCCGACCTCATGGGGTACATcCGCTCGTCGGCGCCCC
103	DK7	367 ATCGATACCCCTTACGTGCGGCTTCGCCGACCTCATGGGGTACATACCGCTCGTCGGCGCCCC
104	US11	367 ATCGATACCCCTTACGTGCGGCTTCGCCGACCTCATGGGGTACATACCGCTCGTCGGCGCCCC
105	S14	367 ATCGATACCCCTCAGTCGGGCTTCGCCGACCTCATGGGGTACATACCGCTCGTCGGCGCCCC
106	SW1	367 ATCGATACCCCTCAGTCGGGCTTCGCCGACCTCATGGGGTACATTCGGCTCGTCGGCGCCCC
107	S18	367 ATCGATACCCCTCAGTCGGGCTTCGCCGACCTCATGGGGTACATTCGGCTCGTCGGCGCCCC
103-108	consensus	ATCGATACCCCTcACGTGCGGCTTCGCCGACCTCATGGGGTACATaCCGCTCGTCGGCGCCCC
SEQ ID NO:	ISOLATE	
108	DR4	428 CcCTTGgGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGaGTTCTGGAAGACGGCGTGAA
103	DK7	428 CTCTTGAGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAAGACGGCGTGAA
104	US11	428 CTCTCGAGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAAGACGGCGTGAA
105	S14	428 CcCTCGgGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAAGACGGCGTGAA
106	SW1	428 CTCTtGGAGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAAGACGGCGTGAA
107	S18	428 CTCTcGGAGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAAGACGGCGTGAA
103-108	consensus	CtCT - GGaGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGgGTTCTGGAAGACGGCGTGAA
SEQ ID NO:	ISOLATE	
108	DR4	489 CTATGCAACAGGGAAtCTTCCTGGTTGCTCTTTCTCTATCTTCCTTTTGGCttTGCTCTCT
103	DK7	489 CTATGCAACAGGGAACCTTCCTGGTTGCTCTTTCTCTATCTTCCTTTTGGCCCTGCTCTCT
104	US11	489 CTATGCAACAGGGAACCTTCCTGGTTGCTCTTTCTCTATCTTCCTTTCTGGCCCTGCTCTCT
105	S14	489 CTATGCAACAGGGAACCTTCCTGGTTGCTCTTTCTCTATCTTCCTcCTaGCCCTGCTTTCT
106	SW1	489 CTATGCAACAGGGAACCTTCCTGGTTGCTCTTTCTCTATCTTCCTTTCTGGCCCTGCTTTCT
107	S18	489 CTATGCAACAGGGAACCTTCCTGGTTGCTCTTTCTCTATCTTCCTTTCTGGCCCTGCTcTCT
103-108	consensus	CTATGCAACAGGGAACCTTCCTGGTTGCTCTTTCTCTATCTTCCTtcTgGccctGCTcTCTCT

NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF
THE ENVELOPE 1...

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FIGURE 6A-4

<u>SEQ ID NO.</u>	<u>ISOLATE</u>	
108	DR4	550 TGctTGACCGTGCCCGCaTcGGCC
103	DK7	550 TGCCTGACCGTGCCCGCTTCGGCC
104	US11	550 TGCCTGACTGTGCCCCGCTTCAGCC
105	S14	550 TGCCTGACTGTGCCCCGCTTCAGCC
106	SW1	550 TGCCTGACaGTGCCCCGCGTCAGCC
107	S18	550 TGtCTGACTGTGCCCCGCGTCAGct
103-108	consensus	TGccTGACTGTGCCCCGctTCaGCC

FIGURE 6B-1

SEQ ID NO:	ISOLATE	
119	S9	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG
117	IND3	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG
118	IND8	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG
111	D1	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG
112	US6	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG
113	P10	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG
114	DK1	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG
115	T10	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG
116	SW2	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG
122	HK4	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG
109	SA10	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG
110	S45	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG
123	P8	1 ATGAGCACGACTCCTAAACCTCAAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG
124	T3	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG
120	HK3	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG
121	HK5	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG
109-124	consensus	ATGAGCACGAATCCTAAACCTCAAAGAAaAaACCAACGTAACACCAaCCGCGGCCACAGG

FIGURE 6B-2

SEQ ID NO:	ISOLATE	
119	S9	62 ACGTCAAGTTCCCGGCGGTGGTCAAGTCGTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
117	IND3	62 ACGTCAAGTTCCCGGCGGTGGTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
118	IND8	62 ACGTCAAGTTCCCGGCGGTGGTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
111	D1	62 ACGTCAAGTTCCCGGCGGTGGTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
112	US6	62 ACGTCAAGTTCCCGGCGGTGGTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
113	P10	62 ACGTCAAGTTCCCGGCGGTGGTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
114	DK1	62 ACGTCAAGTTCCCGGCGGTGGTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
115	T10	62 ACGTCAAGTTCCCGGCGGTGGTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
116	SW2	62 ACGTCAAGTTCCCGGCGGTGGTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
122	HK4	62 ACGTCAAGTTCCCGGCGGTGGTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
109	SA10	62 ACGTCAAGTTCCCGGCGGTGGTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
110	S45	62 ACGTCAAGTTCCCGGCGGTGGTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
123	P8	62 ACGTCAAGTTCCCGGCGGTGGTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
124	T3	62 ACGTCAAGTTCCCGGCGGTGGTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
120	HK3	62 ACGTCAAGTTCCCGGCGGTGGTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
121	HK5	62 ACGTCAAGTTCCCGGCGGTGGTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
109-124	consensus	ACGTCAAGTTCCCGGCGGTGGTGGTGGAGTTTACCTGTTGCCGCGCAGGGG

NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF
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FIGURE 6B-3

SEQ ID NO:	ISOLATE	
119	S9	123 CCCAGGTTGGGTGTGCGCGCaACTAGGAAGACTTCCGAGCGGTCCGAACCTCGTGAAGG
117	IND3	123 CCCAGGTTGGGTGTGCGCGGACTAGGAAGACTTCCGAGCGGTCCGAACCTCGTGAAGG
118	IND8	123 CCCAGGTTGGGTGTGCGCGGACTAGGAAGACTTCCGAGCGGTCCGAACCTCGTGAAGG
111	D1	123 CCCAGGTTGGGTGTGCGCGGACTAGGAAGACTTCCGAGCGGTCCGAACCTCGTGAAGG
112	US6	123 CCCAGGTTGGGTGTGCGCGGACTAGGAAGACTTCCGAGCGGTCCGAACCTCGTGAAGG
113	P10	123 CCCAGGTTGGGTGTGCGCGGACTAGGAAGACTTCCGAGCGGTCCGAACCTCGTGAAGG
114	DK1	123 CCCAGGTTGGGTGTGCGCGGACTAGGAAGACTTCCGAGCGGTCCGAACCTCGTGAAGG
115	T10	123 CCCAGGTTGGGTGTGCGCGGACTAGGAAGACTTCCGAGCGGTCCGAACCTCGTGAAGG
116	SW2	123 CCCcGGTTGGGTGTGCGCGGACTAGGAAGACTTCCGAGCGGTCCGAACCTCGTGAAGG
122	HK4	123 CCCAGGTTGGGTGTGCGCGGACTAGGAAGACTTCCGAGCGGTCCGAACCTCGTGAAGG
109	SA10	123 CCCAGGTTGGGTGTGCGCGGACTAGGAAGACTTCCGAGCGGTCCGAACCTCGTGAAGG
110	S45	123 CCCAGGTTGGGTGTGCGCGGACTAGGAAGACTTCCGAGCGGTCCGAACCTCGTGAAGG
123	P8	123 CCCAGGTTGGGTGTGCGCGGACTAGGAAGACTTCCGAGCGGTCCGAACCTCGTGAAGG
124	T3	123 CCCAGGTTGGGTGTGCGCGGACTAGGAAGACTTCCGAGCGGTCCGAACCTCGTGAAGG
120	HK3	123 CCCAGGTTGGGTGTGCGCGGACTAGGAAGACTTCCGAAGCGGTCCGAACCTCGTGAAGG
121	HK5	123 CCCAGGTTGGGTGTGCGCGGACTAGGAAGACTTCCGAAGCGGTCCGAACCTCGTGAAGG
109-124	consensus	CCCCaGGTTGGGTGTGCGCGGcGACTAGGAAGACTTCCGAGCGgTcGCAACCTCGTGGaaGG

FIGURE 6B-4

SEQ ID NO:	ISOLATE	
119	S9	184 CGACAACCTATCCCCAAGGCTCGCCat CCCGAGGGcAGGGCCTGGGCTCAGCCCGGGTACC
117	IND3	184 CGACAACCTATCCCCAAGGCTCGCCGGCCCGAGGGTAGGGCTGGGCTCAGCCCGGGTACC
118	IND8	184 CGACAACCTATCCCCAAGGCTCGCCGGCCCGAGGGTAGGGCTGGGCTCAGCCCGGGcACC
111	D1	184 CGACAACCTATCCCCAAGGCTCGCCGGCCCGAGGGTAGGGCTGGGCTCAGCCCGGGTACC
112	US6	184 CGACAACCTATCCCCAAGGCTCGCCGGCCCGAGGGTAGGGCTGGGCTCAGCCCGGGTACC
113	P10	184 CGACAACCTATCCCCAAGGCTCGCCGGCCCGAGGGTAGGGCTGGGCTCAGCCCGGGTACC
114	DK1	184 CGACAACCTATCCCCAAGGCTCGCCGGCCCGAGGGTAGGGCTGGGCTCAGCCCGGGTACC
115	T10	184 CGACAACCTATCCCCAAGGCTCGCCAGCCCGAGGGCAGGGCCTGGGCTCAGCCtGGGTACC
116	SW2	184 CGACAACCTATCCCCAAGGCTCGCCAGCCCGAGGGCAGGGCCTGGGCTCAGCCtGGGTACC
122	HK4	184 CGACAACCTATCCCCAAGGCTCGCCaAaCCCGAGGGCAGGACCTGGGCTCAGCCCGGGTACC
109	SA10	184 CGACAACCTATCCCCAAGGCTCGCCAGCCCGAGGGCAGGACCTGGGCCcAGCCCGGGTACC
110	S45	184 CGACAACCTATCCCCAAGGCTCGCCGGCCCGAGGGCAGGGCCTGGGCCcAGCCCGGGCAtC
123	P8	184 CGACAACCTATCCCCAAGGCTCGCCGGCCCGAGGGTAGGGCTGGGCTCAGCCCGGGCACC
124	T3	184 CGACAACCTATCCCCAAGGCTCGCCGGCCCGAGGGTAGGGCTGGGCTCAGCCCGGGTACC
120	HK3	184 CGACAACCTATCCCCAAGGCTCGCCaACCCGAGGGCAGGACCTGGGCTCAGCCCGGGTATC
121	HK5	184 CGACAACCTATCCCCAAGGCTCGCCgACCCGAGGGCAGGACCTGGGCTCAGCCCGGGTATC
109-124	consensus	CGACAaCCTATCCCCCAAGGCTCGCCgGCCGAGGGcAGGgCCTGGGCTCAGCCcGGGtACC

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FIGURE 6B-5

SEQ ID NO.:	ISOLATE	
119	S9	245 CTTGGCCCCCTCTACGGCAATGAGGGCTTGGGTTGGCAGGATGGCTCCTGTCAACCCCGTGG
117	IND3	245 CTTGGCCCCCTCTATGGCAATGAGGGCTTGGGTTGGCAGGATGGCTCCTGTCAACCCCGCGG
118	IND8	245 CTTGGCCCCCTCTATGGCAATGAGGGCTTGGGTTGGCAGGATGGCTCCTGTCAACCCCGCGG
111	D1	245 CTTGGCCCCCTCTATGGCAACGAGGGCTTGGGTTGGCAGGATGGCTCCTGTCAACCCCGCGG
112	US6	245 CTTGGCCCCCTCTATGGCAACGAGGGCaTGGGTTGGCAGGATGGCTCCTGTCAACCCCGTGG
113	P10	245 CTTGGCCCCCTCTATGGCAATGAGGGCTTGGGTTGGCAGGATGGCTCCTGTCAACCCCGTGG
114	DK1	245 CTTGGCCCCCTCTATGGCAATGAGGGCTTGGGTTGGCAGGATGGCTCCTGTCAACCCCGCGG
115	T10	245 CTTGGCCCCCTCTATGGCAATGAGGGCTTGGGTTGGCAGGATGGCTCCTGTCAACCCCGTGG
116	SW2	245 CcTTGGCCCCCTCTATGGCAATGAGGGCTTGGGTTGGCAGGATGGCTCCTGTCAACCCCGCGG
122	HK4	245 CTTGGCCCCCTCTATGGCAATGAGGGCTTGGGTTGGCAGGATGGCTCCTGTCAACCCCGCGG
109	SA10	245 CTTGGCCCCCTCTATGGCAATGAGGGCTTGGGTTGGCAGGATGGCTCCTGTCAACCCCGTGG
110	S45	245 CTTGGCCCCCTCTATGGCAATGAGGGCTTGGGTTGGCAGGATGGCTCCTGTCAACCCCGTGG
123	P8	245 CTTGGCCCCCTCTATGcCAATGAGGGCTTGGGTTGGGgGGATGGCTCCTGTCAACCCCGCGG
124	T3	245 CTTGGCCCCCTCTATGGCGACGAGGGCTTGGGTTGGGgGGATGGCTCCTGTCAACCCCGCGG
120	HK3	245 CTTGGCCCCCTCTATGGCAACGAGGGCTTGGGTTGGCAGGATGGCTCCTGTCAACCCCGCGG
121	HK5	245 CTTGGCCCCCTCTATGGCAATGAGGGCTTGGGTTGGCAGGATGGCTCCTGTCAACCCCGTGG
109-124	consensus	CtTTGGCCCCCTCTAtGgCaAtGAGGGC - TGGGgTGGGCaGATGGCTCCTGTCTcTGTcACCCCGCGG

FIGURE 6B-6

SEQ ID NO:	ISOLATE	
119	S9	306 cTCTCGGCCTAGTTGGGGCCCCAatGACCCCCCGCGTAGGTCGCGTAATTTGGGTAAGGTC
117	IND3	306 tTCTCGGCCTAGTTGGGGCCCCCAGACCCCCCGCGTAGGTCGCGTAATTTGGGTAAGGTC
118	IND8	306 CTCTCGGCCTAGTTGGGGCCCCCAGACCCCCCGCGTAGGTCGCGTAATTTGGGTAAGGTC
111	D1	306 CTCCCGGCCTAGTTGGGGCCCCCAGACCCCCCGCGTAGGTCGCGTAATTTGGGTAAGGTC
112	US6	306 CTCCCGGCCTAGTTGGGGCCCCCAGGACCCCCCGCGTAGGTCGCGTAATTTGGGTAAGGTC
113	P10	306 CTCTCGGCCTAGTTGGGGCCCCCAGGACCCCCCGCGTAGGTCGCGTAATTTGGGTAAGGTC
114	DK1	306 CTCTCGGCCTAGTTGGGGCCCCCAGACCCCCCGCGTAGGTCGCGTAATTTGGGTAAGGTC
115	T10	306 CTCcCGGCCTAGTTGGGGCCCCCAGACCCCCCGCGTAGGTCGCGTAATTTGGGTAAGGTC
116	SW2	306 CTCTCGGCCTAGTTGGGGCCCCCAGACCCCCCGCGTAGGTCGCGTAATTTGGGTAAGGTC
122	HK4	306 CTCTCGGCCTAGTTGGGGCCCCCAGGACCCCCCGCGTAGGTCGCGTAATTTGGGTAAGGTC
109	SA10	306 CTCTCGGCCTAGTTGGGGCCCCCAGGACCCCCCGCGTAGGTCGCGTAATTTGGGTAAGGTC
110	S45	306 CTCTCGGCCTAGTTGGGGCCCCCAGGACCCCCCGCGTAGGTCGCGTAATTTGGGTAAGGTC
123	P8	306 CTCCCGGCCTAGTTGGGGCCCCCAGGACCCCCCGCGTAGGTCGCGTAATTTGGGTAAGGTC
124	T3	306 CTCCCGGCCTAATTTGGGGCCCCCAGACCCCCCGCGTAGGTCGCGTAATTTGGGTAAGGTC
120	HK3	306 CTCTCGGCCTAATTTGGGGCCCCCAGGACCCCCCGCGTAGGTCGCGTAATTTGGGTAAGGTC
121	HK5	306 CTCTCGGCCTAgTTGGGGCCCCCAGGACCCCCCGCGTAGGTCGCGTAATTTGGGTAAGGTC
109-124	consensus	cTCTcCGGCCTAgTTGGGGCCCCCAGGACCCCCCGCGTAGGTCGCGTAATTTGGGTAAGGTC

FIGURE 6B-7

SEQ ID NO:	ISOLATE	
119	S9	367 ATCGATACCCCTCACATGCGGCTTtGCCGACCTCATGGGGTACATtCCGCTCGTCGGCGCCCC
117	IND3	367 ATCGATACCCCTCACATGCGGCTTtGCCGACCTCATGGGGTACATtCCGCTCGTCGGCGCCCC
118	IND8	367 ATCGATACCCCTCACATGCGGCTTtGCCGACCTCATGGGGTACATtCCGCTCGTCGGCGCCCC
111	D1	367 ATCGATACCCCTCACATGCGGCTTtGCCGACCTCATGGGGTACATtCCGCTCGTCGGCGCCCC
112	US6	367 ATCGATACCCCTCACATGCGGCTTtGCCGACCTCATGGGGTACATtCCGCTCGTCGGCGCCCC
113	P10	367 ATCGATACCCCTCACATGCGGCTTtGCCGACCTCATGGGGTACATtCCGCTCGTCGGCGCCCC
114	DK1	367 ATCGATACCCCTCACATGCGGCTTtGCCGACCTCATGGGGTACATtCCGCTCGTCGGCGCCCC
115	T10	367 ATCGATACCCCTCACATGCGGCTTtGCCGACCTCATGGGGTACATtCCGCTCGTCGGCGCCCC
116	SW2	367 ATCGATACCCCTCACATGCGGCTTtGCCGACCTCATGGGGTACATtCCGCTCGTCGGCGCCCC
122	HK4	367 ATCGATACCCCTCACATGCGGCTTtGCCGACCTCATGGGGTACATtCCGCTCGTCGGCGCCCC
109	SA10	367 ATCGATACCCCTCACATGCGGCTTtGCCGACCTCATGGGGTACATtCCGCTCGTCGGCGCCCC
110	S45	367 ATCGATACCCCTCACgTGCGGCTTtGCCGACCTCATGGGGTACATtCCGCTCGTCGGCGCCCC
123	P8	367 ATCGATACCCCTCACATGCGGCTTtGCCGACCTCATGGGGTACATtCCGCTCGTCGGCGGgCC
124	T3	367 ATCGATACCCCTCACATGCGGCTTtGCCGACCTCATGGGGTACATtCCGCTCGTCGGCGGctC
120	HK3	367 ATCGATACCCCTCACGTGCGGCTTtGCCGACCTCATGGGGTACATtCCGCTCGTCGGtGCC
121	HK5	367 ATCGATACCCCTCACGTGCGGCTTtGCCGACCTCATGGGGTACATtCCGCTCGTCGGcGCC
109-124	consensus	ATCGATACCCCTCACaTGCGGCTTtGCCGACCTCATGGGGTACATtCCGCTCGTCGGcGccc

FIGURE 6B-8

SEQ ID NO:	ISOLATE	
119	S9	428 CCCTAGGGGGCGCTGCCAGGGCtCTGGCGCATGGCGTCCGGTtCTGGAGGACGGCGTGAA
117	IND3	428 CCCTAGGGGGCGCTGCCAGGGCCTGGCGCATGGCGTCCGGTcCTGGAGGACGGCGTGAA
118	IND8	428 CCCTAGGGGGTGTCTGCCAGGGCCTGGCGCATGGCGTCCGGTcCTGGAGGACGGCGTGAA
111	D1	428 CCCTAGGGGGTGTCTGCCAGGGCCTGGCGCATGGCGTCCGGTtCTGGAGGACGGCGTGAA
112	US6	428 CCCTAGGGGGCGCTGCCAGGGCCTGGCGCATGGCGTCCGGTtCTGGAGGACGGCGTGAA
113	P10	428 CCCTAGGGGGCGCTGCCAGGGCCTGGCGCATGGCGTCCGGTtCTGGAGGACGGCGTGAA
114	DK1	428 CCCTAGGGGGCGCTGCCAGGGCCTGGCGCATGGCGTCCGGTtCTGGAGGACGGCGTGAA
115	T10	428 CCCTAGGGGGCGCTGCCAGGGCCTGGCGCATGGCGTCCGGTtCTGGAGGACGGCGTGAA
116	SW2	428 CCCTAGGGGGCGCTGCCAGGGCCTGGCGCATGGCGTCCGGTtCTGGAGGACGGCGTGAA
122	HK4	428 CCCTAGGGGGCGTGCAGAGCCCTGGCaCATGGtGTCCGGTtCTGGAGGACGGCGTGAA
109	SA10	428 CtTTAGGGGGCGCTGCCAGGcCTTGGCGCATGGCGTCCGGTtCTGGAGGACGGCGTGAA
110	S45	428 CCCTAGGGGGCGCTGCCAGAGCCtTGGCGCATGGCGTCCGGTtCTGGAGGACGGCGTGAA
123	P8	428 CCCTAGGGGGCGTtGCCAGGGCCTTGGCGCATGGCGTCCGGTtTgTGGAGGACGGCGTGAA
124	T3	428 CCtTAGGGGGCGTtGCCAGGGCCTTGGCGCATGGCGTCCGGTtCTGGAGGACGGCGTGAA
120	HK3	428 CCCTAGGGGGCGTtGCCAGAGCctTGGCaCATGGTGTCCGGTtCTGGAGGACGGCGTGAA
121	HK5	428 CCCTAGGGGGCGTtGCCAGAGCCcTGGCaCACGGTGTCCGGTtCTGGAGGACGGCGTGAA
109-124	consensus	CccTAGGGGGcGcTGCCAGgGCccTGGCgCatGGcGTCCGGGtTcTGGAGgACGGCGTGAA

FIGURE 6B-9

SEQ ID NO:	ISOLATE	
119	S9	CTATGCAACAGGGAACcTcCCCGGTGGCTCTTTCTCTATCTTCCTcTgGCTTTGCTgTCC
117	IND3	CTATGCAACAGGGAACcTGGCCCGGTGGCTCTTTCTCTATCTTCCTTTAGCTTTGCTATCC
118	IND8	CTATGCAACAGGGAACcTGGCCCGGTGGCTCTTTCTCTATCTTCCTTTGGCTTTGCTATCC
111	D1	tTATGCAACAGGGAAtTTGCCCGGTGGCTCTTTCTCTATCTTCCTCTTGGCTTTGCTGTCC
112	US6	CTATGCAACAGGGAACcTGGCCCGGTGGCTCTTTCTCTATCTTCCTCTTGGCTTTGCTGTCC
113	P10	CTATGCAACAGGGAAtcTGGCCCGGTGGCTCTTTCTCTATCTTCCTCTTGGCTTTGCTGTCC
114	DK1	CTACGCAACAGGGAATTTGCCCGGTGGCTCTTTCTCTATCTTCCTCTTGGCTCTGTgTCC
115	T10	CTATGCAACAGGGAATTTGCCCGGTGGCTCTTTCTCTATCTTCCTCTTGGCTCTGTGTCT
116	SW2	CTATGCAACAGGGAAtcTGGCCCGGTGGCTCTTTCTCTATCTTCCTCTTGGCTcTGTGTCC
122	HK4	CTATGCAACAGGGAATTTGCCCGGTGGCTCTTTCTCTATCTTCCTCTTGGCTcTGTGTCC
109	SA10	CTATGCAACAGGGAATTTGCCCGGTGGCTCTTTCTCTATCTTCCTCTTGGCTcTGTGTCC
110	S45	CTATGCAACAGGGAATcTGGCCCGGTGGCTCTTTCTCTATCTTCCTCTTGGCTcTGTGTCC
123	P8	CTATGCAACAGGGAATcTGGCTGGTGGCTCTTTCTCTATCTTCCTCTTGGCTTTGCTGTCT
124	T3	tTACGCAACAGGGAATTTGCCCTGGTGGCTCTTTCTCTATCTTCCTCTTGGCTTTGCTGTCC
120	HK3	CTATGCAACAGGGAATTTACCCGGTGGCTCTTTCTCTATCTTCCTCTTGGCTTTGCTGTCC
121	HK5	CTACGCAACAGGGAAtaTACCCGGTGGCTCTTTCTCTATCTTCCTcTTGGCTTTGCTGTCC
109-124	consensus	cTAtGCAACAGGGAAttTgCCcGGTtGCTcTtTcTCTATCTTCCTctTgGCTtTgCTgTCC

FIGURE 6B-10

SEQ ID NO:	ISOLATE	
119	S9	550 TGTTTGACCATCCAGCTTCCGCT
117	IND3	550 TGTTTGACCATCCAGCTTCCGCT
118	IND8	550 TGTTTGACCGTCCAGCTTCCGCT
111	D1	550 TGTTTGACCATCCAGCTTCCGCT
112	US6	550 TGTTTGACCATCCAGCTTCCGCT
113	P10	550 TGccTGACCATCCAGCGTCCGCT
114	DK1	550 TGTTTGACCATCCAGCTTCCGcc
115	T10	550 TGTCTGACCATCCAGCTTCCGCT
116	SW2	550 TGTCTGACCATCCAGCTTCCGCT
122	HK4	550 TGTTTGACCATCCAGCTTCCGCT
109	SA10	550 TGTTTaACCATCCAGCTTCCGCT
110	S45	550 TGctTGACCATCCAGCTTCCGCT
123	P8	550 TGtcTGACCATCCAGCTTCCGCT
124	T3	550 TGCTTGACCATCCAGCTTCCGCT
120	HK3	550 TGCTTGACCACCCCAGCTTCCGCT
121	HK5	550 TGtcTGACCACCCCAGtTCCGCT
109-124	consensus	TGttTgACCatcCCAGctTCCGct

FIGURE 6C-1

SEQ ID NO:	ISOLATE	
119	S9	1 ATGAGCACGAATCCTAAACCTCAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG
117	IND3	1 ATGAGCACGAATCCTAAACCTCAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG
118	IND8	1 ATGAGCACGAATCCTAAACCTCAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG
111	D1	1 ATGAGCACGAATCCTAAACCTCAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG
112	US6	1 ATGAGCACGAATCCTAAACCTCAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG
113	P10	1 ATGAGCACGAATCCTAAACCTCAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG
114	DK1	1 ATGAGCACGAATCCTAAACCTCAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG
115	T10	1 ATGAGCACGAATCCTAAACCTCAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG
116	SW2	1 ATGAGCACGAATCCTAAACCTCAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG
122	HK4	1 ATGAGCACGAATCCTAAACCTCAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG
109	SA10	1 ATGAGCACGAATCCTAAACCTCAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG
110	S45	1 ATGAGCACGAATCCTAAACCTCAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG
123	P8	1 ATGAGCACGAATCCTAAACCTCAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG
124	T3	1 ATGAGCACGAATCCTAAACCTCAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG
120	HK3	1 ATGAGCACGAATCCTAAACCTCAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG
121	HK5	1 ATGAGCACGAATCCTAAACCTCAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG
108	DR4	1 ATGAGCACGAATCCTAAACCTCAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG
104	US11	1 ATGAGCACGAATCCTAAACCTCAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG
105	S14	1 ATGAGCACGAATCCTAAACCTCAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG
106	SW1	1 ATGAGCACGAATCCTAAACCTCAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG
107	S18	1 ATGAGCACGAATCCTAAACCTCAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG
103	DK7	1 ATGAGCACGAATCCTAAACCTCAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG
103-124	consensus	ATGAGCACGAATCCTAAACCTCAAGAAAAACCAACGTAACACCAACCGCGGCCACAGG

FIGURE 6C-2

SEQ ID NO:	ISOLATE	
119	S9	62 ACGTCAAGTTC
117	IND3	62 ACGTCAAGTTC
118	IND8	62 ACGTCAAGTTC
111	D1	62 ACGTCAAGTTC
112	US6	62 ACGTCAAGTTC
113	P10	62 ACGTCAAGTTC
114	DK1	62 ACGTCAAGTTC
115	T10	62 ACGTCAAGTTC
116	SW2	62 ACGTCAAGTTC
122	HK4	62 ACGTCAAGTTC
109	SA10	62 ACGTCAAGTTC
110	S45	62 ACGTCAAGTTC
123	P8	62 ACGTCAAGTTC
124	T3	62 ACGTCAAGTTC
120	HK3	62 ACGTCAAGTTC
121	HK5	62 ACGTCAAGTTC
108	DR4	62 ACGTCAAGTTC
104	US11	62 ACGTCAAGTTC
105	S14	62 ACGTCAAGTTC
106	SW1	62 ACGTCAAGTTC
107	S18	62 ACGTCAAGTTC
103	DK7	62 ACGTCAAGTTC
103-124	consensus	ACGTCAAGTTC

FIGURE 6C-3

SEQ ID NO:	ISOLATE	
119	S9	123 CCCAGGTTGGGTGTGCGCGCaACTAGGAAGACTTCCGAGCGGTGCGAACTCGTGGAAAGG
117	IND3	123 CCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTGCGAACTCGTGGAAAGG
118	IND8	123 CCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTGCGAACTCGTGGAAAGG
111	D1	123 CCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTGCGAACTCGTGGAAAGG
112	US6	123 CCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTGCGAACTCGTGGAAAGG
113	P10	123 CCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTGCGAACTCGTGGAAAGG
114	DK1	123 CCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTGCGAACTCGTGGAAAGG
115	T10	123 CCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTGCGAACTCGTGGAAAGG
116	SW2	123 CCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTGCGAACTCGTGGAAAGG
122	HK4	123 CCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTGCGAACTCGTGGAAAGG
109	SA10	123 CCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTGCGAACTCGTGGAAAGG
110	S45	123 CCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTGCGAACTCGTGGAAAGG
123	P8	123 CCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTGCGAACTCGTGGAAAGG
124	T3	123 CCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTGCGAACTCGTGGAAAGG
120	HK3	123 CCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTGCGAACTCGTGGAAAGG
121	HK5	123 CCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTGCGAACTCGTGGAAAGG
108	DR4	123 CCTAGATTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTGCGAACTCGAGGTAGA
104	US11	123 CCTAGATTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTGCGAACTCGAGGTAGA
105	S14	123 CCTAGATTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTGCGAACTCGAGGTAGA
106	SW1	123 CCTAGATTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTGCGAACTCGAGGTAGA
107	S18	123 CCTAGATTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTGCGAACTCGAGGTAGA
103	DK7	123 CCTAGATTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTGCGAACTCGAGGTAGA
103-124	consensus	CCCcAGTTGGGTGTGCGCGCGaCtAGGAAGACTTcGAGCGgTcGCAACCTCGtGGaaGg

FIGURE 6C-4

SEQ ID NO:	ISOLATE	
119	S9	184 CGACAACCTATCCCCAAGGTCGCatCCCCAGGGcAGGGCCTGGGCTCAGCCCGGGTACC
117	IND3	184 CGACAACCTATCCCCAAGGTCGCGGCCCGAGGGTAGGGCTGGGCTCAGCCCGGGTACC
118	IND8	184 CGACAACCTATCCCCAAGGTCGCGGCCCGAGGGTAGGGCTGGGCTCAGCCCGGGcACC
111	D1	184 CGACAACCTATCCCCAAGGTCGCGGCCCGAGGGTAGGGCTGGGCTCAGCCCGGGTACC
112	US6	184 CGACAACCTATCCCCAAGGTCGCGGCCCGAGGGTAGGGCTGGGCTCAGCCCGGGTACC
113	P10	184 CGACAACCTATCCCCAAGGTCGCGGCCCGAGGGTAGGGCTGGGCTCAGCCCGGGTACC
114	DK1	184 CGACAACCTATCCCCAAGGTCGCGGCCCGAGGGTAGGGCTGGGCTCAGCCCGGGTACC
115	T10	184 CGACAACCTATCCCCAAGGTCGCGGCCCGAGGGTAGGGCTGGGCTCAGCCCGGGTACC
116	SW2	184 CGACAACCTATCCCCAAGGTCGCGGCCCGAGGGTAGGGCTGGGCTCAGCCtGGGTACC
122	HK4	184 CGACAACCTATCCCCAAGGTCGCAaCCCCAGGGCAGGACCTGGGCTCAGCCCGGGTACC
109	SA10	184 CGACAACCTATCCCCAAGGTCGCGGCCCGAGGGTAGGGCTGGGCTCAGCCCGGGTACC
110	S45	184 CGACAACCTATCCCCAAGGTCGCGGCCCGAGGGTAGGGCTGGGCTCAGCCCGGGCAtC
123	P8	184 CGACAACCTATCCCCAAGGTCGCGGCCCGAGGGTAGGGCTGGGCTCAGCCCGGGCACC
124	T3	184 CGACAACCTATCCCCAAGGTCGCGGCCCGAGGGTAGGGCTGGGCTCAGCCCGGGTACC
120	HK3	184 CGACAACCTATCCCCAAGGTCGCAaCCCCAGGGCAGGACCTGGGCTCAGCCCGGGTATC
121	HK5	184 CGACAACCTATCCCCAAGGTCGCGACCCCCAGGGCAGGACCTGGGCTCAGCCCGGGTATC
108	DR4	184 CGTCAGCCTATCCCCAAGGCGCGTCGCGGCCCGAGGGCAGGACCTGGGCTCAGCCCGGGTACC
104	US11	184 CGTCAGCCTATCCCCAAGGCGCGTCGCGGCCCGAGGGCAGGACCTGGGCTCAGCCCGGGTACC
105	S14	184 CGTCAGCCTATCCCCAAGGCGCGTCGCGGCCCGAGGGCAGGACCTGGGCTCAGCCCGGGTATC
106	SW1	184 CGTCAGCCTATCCCCAAGGCGCGTCGCGGCCCGAGGGCAGGACCTGGGCTCAGCCCGGGTATC
107	S18	184 CGTCAGCCTATCCCCAAGGCGCGTCGCGGCCCGAGGGCAGGACCTGGGCTCAGCCCGGGTACC
103	DK7	184 CGTCAGCCTATCCCCAAGGCGaCGTCGCGGCCCGAGGGCAGGACCTGGGCTCAGCCCGGGTACC
103-124	consensus	CGaCAaCCTATCCCCAAGGCTCGcCgCCCCAGGGcAGGgCCTGGGCTCAGCCcGGGtAcc

FIGURE 6C-5

SEQ ID NO:	ISOLATE	
119	S9	245 CTTGGCCCCCTCTA
117	IND3	245 CTTGGCCCCCTCTATGGCAATGAGGGCTTGGGGTGGGAGGATGGCTCCTGTACCCCCGCGG
118	IND8	245 CTTGGCCCCCTCTATGGCAATGAGGGCTTGGGGTGGGAGGATGGCTCCTGTACCCCCGCGG
111	D1	245 CTTGGCCCCCTCTATGGCAACGAGGGCTTGGGGTGGGAGGATGGCTCCTGTACCCCCGCGG
112	US6	245 CTTGGCCCCCTCTATGGCAACGAGGGCTTGGGGTGGGAGGATGGCTCCTGTACCCCCGCGG
113	P10	245 CTTGGCCCCCTCTATGGCAATGAGGGCTTGGGGTGGGAGGATGGCTCCTGTACCCCCGCGG
114	DK1	245 CTTGGCCCCCTCTATGGCAATGAGGGCTTGGGGTGGGAGGATGGCTCCTGTACCCCCGCGG
115	T10	245 CTTGGCCCCCTCTATGGCAATGAGGGCTTGGGGTGGGAGGATGGCTCCTGTACCCCCGCGG
116	SW2	245 CcTTGGCCCCCTCTATGGCAATGAGGGCTTGGGGTGGGAGGATGGCTCCTGTACCCCCGCGG
122	HK4	245 CTTGGCCCCCTCTATGGCAATGAGGGCTTGGGGTGGGAGGATGGCTCCTGTACCCCCGCGG
109	SA10	245 CTTGGCCCCCTCTATGGCAATGAGGGCTTGGGGTGGGAGGATGGCTCCTGTACCCCCGCGG
110	S45	245 CTTGGCCCCCTCTATGGCAATGAGGGCTTGGGGTGGGAGGATGGCTCCTGTACCCCCGCGG
123	P8	245 CTTGGCCCCCTCTATGcCAATGAGGGCTTGGGGTGGGAGGATGGCTCCTGTACCCCCGCGG
124	T3	245 CTTGGCCCCCTCTATGGCGACGAGGGCTTGGGGTGGGAGGATGGCTCCTGTACCCCCGCGG
120	HK3	245 CTTGGCCCCCTCTATGGCAACGAGGGCTTGGGGTGGGAGGATGGCTCCTGTACCCCCGCGG
121	HK5	245 CTTGGCCCCCTCTATGGCAATGAGGGCTTGGGGTGGGAGGATGGCTCCTGTACCCCCGCGG
108	DR4	245 CTTGGCCCCCTCTATGGCAATGAGGGCTTGGGGTGGGAGGATGGCTCCTGTACCCCCGCGG
104	US11	245 CTTGGCCCCCTCTATGGCAATGAGGGCTTGGGGTGGGAGGATGGCTCCTGTACCCCCGCGG
105	S14	245 CTTGGCCCCCTCTATGGCAATGAGGGCTTGGGGTGGGAGGATGGCTCCTGTACCCCCGCGG
106	SW1	245 CTTGGCCCCCTCTATGGCAATGAGGGCTTGGGGTGGGAGGATGGCTCCTGTACCCCCGCGG
107	S18	245 CTTGGCCCCCTCTATGGCAATGAGGGCTTGGGGTGGGAGGATGGCTCCTGTACCCCCGCGG
103	DK7	245 CTTGGCCCCCTCTATGGCAATGAGGGCTTGGGGTGGGAGGATGGCTCCTGTACCCCCGCGG
103-124	consensus	CtTGGCCCCCTCTATgCaAtGAGGGCcttgGgTGGGCaGgATGGCTCCTGTCaCCCCgtGG

FIGURE 6C-6

SEQ ID NO:	ISOLATE	
119	S9	306 cTCTCGGCCTAGTTGGGGCCCCAaTGACCCCGCGGTAGTGCCTAAATTGGGTAAGGTC
117	IND3	306 tTCTCGGCCTAGTTGGGGCCCCACAGACCCCGCGGTAGTGCCTAAATTGGGTAAGGTC
118	IND8	306 CTCTCGGCCTAGTTGGGGCCCCACAGACCCCGCGGTAGTGCCTAAATTGGGTAAGGTC
111	D1	306 CTCCCGGCCTAGTTGGGGCCCCACcGACCCCGCGGTAGTGCCTAAATTGGGTAAGGTC
112	US6	306 CTCCCGGCCTAGTTGGGGCCCCACGGAACCCCGCGGTAGTGCCTAAATTGGGTAAGGTC
113	P10	306 CTCTCGGCCTAGTTGGGGCCCCACGGAACCCCGCGGTAGTGCCTAAATTGGGTAAGGTC
114	DK1	306 CTCTCGGCCTAGTTGGGGCCCCAaCGACCCCGCGGTAGTGCCTAAATTGGGTAAGGTC
115	T10	306 CTCcCGGCCTAGTTGGGGCCCCACaGACCCCGCGGTAGTGCCTAAATTGGGTAAGGTC
116	SW2	306 CTCTCGGCCTAGTTGGGGCCCCACtGACCCCGCGGTAGTGCCTAAATTGGGTAAGGTC
122	HK4	306 CTCTCGGCCTAGTTGGGGCCCCACGGAACCCCGCGGTAGTGCCTAAATTGGGTAAGGTC
109	SA10	306 CTCTCGGCCTAGTTGGGGCCCCACGGAACCCCGCGGTAGTGCCTAAATTGGGTAAGGTC
110	S45	306 CTCCCGGCCTAGTTGGGGCCCCACGGAACCCCGCGGTAGTGCCTAAATTGGGTAAGGTC
123	P8	306 CTCCCGGCCTAGTTGGGGCCCCACGGAACCCCGCGGTAGTGCCTAAATTGGGTAAGGTC
124	T3	306 CTCCCGGCCTAAATTGGGGCCCCACaGACCCCGCGGTAGTGCCTAAATTGGGTAAGGTC
120	HK3	306 CTCTCGGCCTAAATTGGGGCCCCACGGAACCCCGCGGTAGTGCCTAAATTGGGTAAGGTC
121	HK5	306 CTCTCGGCCTAGTTGGGGCCCCACGGAACCCCGCGGTAGTGCCTAAATTGGGTAAGGTC
108	DR4	306 CTCTCGGCCTAGTGGGGCCCCACaGACCCCGCGGTAGTGCCTAAATTGGGTAAGGTC
104	US11	306 CTCTCGGCCTAGTGGGGCCCCACgGACCCCGCGGTAGTGCCTAAATTGGGTAAGGTC
105	S14	306 CTCTCGGCCTAGTGGGGCCCCACAGACCCCGCGGTAGTGCCTAAATTGGGTAAGGTC
106	SW1	306 CTCTCGGCCTAGTGGGGCCCCTACAGACCCCGCGGTAGTGCCTAAATTGGGTAAGGTC
107	S18	306 CTCcCGGCCTAGTGGGGCCCCTACAGACCCCGCGGTAGTGCCTAAATTGGGTAAGGTC
103	DK7	306 CTCTCGGCCTAGTGGGGCCCCcACAGACCCCGCGGTAGTGCCTAAATTGGGTAAGGTC
103-124	consensus	cTCTCGGCCTAgTGGGGCCCCAc - GACCCCGCGGTAGTGCCTAAATTGGGTAAGGTC

FIGURE 6C-7

SEQ ID NO:	ISOLATE	
119	S9	367 ATCGATACCCCTCACATGCGGCTTtGCCGACCTCATGCGGTACATtCCGCTCGTCGGCGCCC
117	IND3	367 ATCGATACCCCTCACATGCGGCTTtGCCGACCTCATGCGGTACATtCCGCTCGTCGGCGCCC
118	IND8	367 ATCGATACCCCTCACATGCGGCTTtGCCGACCTCATGCGGTACATtCCGCTCGTCGGCGCCC
111	D1	367 ATCGATACCCCTCACATGCGGCTTtGCCGACCTCATGCGGTACATtCCGCTCGTCGGCGCCC
112	US6	367 ATCGATACCCCTCACATGCGGCTTtGCCGACCTCATGCGGTACATtCCGCTCGTCGGCGCCC
113	P10	367 ATCGATACCCCTCACATGCGGCTTtGCCGACCTCATGCGGTACATtCCGCTCGTCGGCGCCC
114	DK1	367 ATCGATACCCCTCACATGCGGCTTtGCCGACCTCATGCGGTACATtCCGCTCGTCGGCGCCC
115	T10	367 ATCGATACCCCTCACATGCGGCTTtGCCGACCTCATGCGGTACATtCCGCTCGTCGGCGCCC
116	SW2	367 ATCGATACCCCTCACATGCGGCTTtGCCGACCTCATGCGGTACATtCCGCTCGTCGGCGCCC
122	HK4	367 ATCGATACCCCTCACATGCGGCTTtGCCGACCTCATGCGGTACATtCCGCTCGTCGGCGCCC
109	SA10	367 ATCGATACCCCTCACATGCGGCTTtGCCGACCTCATGCGGTACATtCCGCTCGTCGGCGCCC
110	S45	367 ATCGATACCCCTCACgTGGGCTTtGCCGACCTCATGCGGTACATtCCGCTCGTCGGCGCCC
123	P8	367 ATCGATACCCCTCACATGCGGCTTtGCCGACCTCATGCGGTACATtCCGCTCGTCGGCGGCC
124	T3	367 ATCGATACCCCTCACATGCGGCTTtGCCGACCTCATGCGGTACATtCCGCTCGTCGGCGGctC
120	HK3	367 ATCGATACCCCTCACGTGGGCTTtGCCGACCTCATGCGGTACATtCCGCTCGTCGGtGCC
121	HK5	367 ATCGATACCCCTCACGTGGGCTTtGCCGACCTCATGCGGTACATtCCGCTCGTCGGCGCCC
108	DR4	367 ATCGAcACCCCTCACGTGGGCTTtGCCGACCTCATGCGGTACATtCCGCTCGTCGGCGCCC
104	US11	367 ATCGATACCCCTtACGTGGGCTTtGCCGACCTCATGCGGTACATtCCGCTCGTCGGCGCCC
105	S14	367 ATCGATACCCCTCACGTGGGCTTtGCCGACCTCATGCGGTACATtCCGCTCGTCGGCGCCC
106	SW1	367 ATCGATACCCCTCACGTGGGCTTtGCCGACCTCATGCGGTACATtCCGCTCGTCGGCGCCC
107	S18	367 ATCGATACCCCTCACGTGGGCTTtGCCGACCTCATGCGGTACATtCCGCTCGTCGGCGCCC
103	DK7	367 ATCGATACCCCTtACGTGGGCTTtGCCGACCTCATGCGGTACATtCCGCTCGTCGGCGCCC
103-124	consensus	ATCGATACCCCTcACaTGGGGCTTtGCCGACCTCATGCGGTACATtCCGCTCGTCGGcGccc

FIGURE 6C-8

SEQ ID NO:	ISOLATE	
119	S9	428 CCCTAGGGGGCGCTGCCAGGGCtCTGGCGCATGGCGTCCGGGTtCTGGAGGACGGCGTGAA
117	IND3	428 CCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTtCTGGAGGACGGCGTGAA
118	IND8	428 CCCTAGGGGGTGTGCCAGGGCCCTGGCGCATGGCGTCCGGGTtCTGGAGGACGGCGTGAA
111	D1	428 CCCTAGGGGGTGTGCCAGGGCCCTGGCGCATGGCGTCCGGGTtCTGGAGGACGGCGTGAA
112	US6	428 CCCTAGGGGGCGCTGCCAGGGCctTGGCGCATGGCGTCCGGGTtCTGGAGGACGGCGTGAA
113	P10	428 CCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTtCTGGAGGACGGCGTGAA
114	DK1	428 CCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTtCTGGAGGACGGCGTGAA
115	T10	428 CCCTAGGGGGCGCTGCCAGGGctCTGGCaCATGGtGTCCGGGTtCTGGAGGACGGCGTGAA
116	SW2	428 CCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTtCTGGAGGACGGCGTGAA
122	HK4	428 CcTTAGGGGGCGtTGCcAGAGCCCTGGCGCATGGCGTCCGGGTtTgTGGAGGACGGCGTGAA
109	SA10	428 CtTTAGGGGGCGCTGCCAGAGcCCCTGGCGCATGGCGTCCGGGTtTGGAGGACGGCGTGAA
110	S45	428 CCCTAGGGGGCGCTGCCAGAGcCCCTGGCGCATGGCGTCCGGGTtCTGGAGGACGGCGTGAA
123	P8	428 CCCTAGGGGGCGTtTGCcAGGGCCCTGGCGCATGGCGTCCGGGTtTgTGGAGGACGGCGTGAA
124	T3	428 CctTAGGGGGCGTtTGCcAGGGCCCTGGCGCATGGCGTCCGGGTtTgTGGAGGACGGCGTGAA
120	HK3	428 CCCTAGGGGGCGTtTGCcAGAGCCtTGGCACATGGTGTCCGGGTtCTGGAGGACGGCGTGAA
121	HK5	428 CCCTAGGGGGCGTtTGCcAGAGCCCTGGCACAGGTGTCCGGGTtCTGGAGGACGGCGTGAA
108	DR4	428 CCCTtGGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGaGtTCTGGAAGACGGCGTGAA
104	US11	428 CtCTCGGaGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTtCTGGAAGACGGCGTGAA
105	S14	428 CcCTCGGgGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTtCTGGAAGACGGCGTGAA
106	SW1	428 CTCTtGGAGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTtCTGGAAGACGGCGTGAA
107	S18	428 CTCTcGGAGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTtCTGGAAGACGGCGTGAA
103	DK7	428 CTCTtGGAGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTtCTGGAAGACGGCGTGAA
103-124	consensus	CccTaGGgGgcGcTGCCAGgGccTGGCgCaTGGcGTCCGgGTtCTGGAgGACGGCGTGAA

FIGURE 6C-9

SEQ ID NO:	ISOLATE	
119	S9	CTATGCAACAGGGAACcTCCCCGGTTGCTCTTTCTCTATCTTCCCTTcTgGCTTTGCTgTCC
117	IND3	CTATGCAACAGGGAACcTTGCCCGGTTGCTCTTTCTCTATCTTCCCTTTaGCTTTGCTATCC
118	IND8	CTATGCAACAGGGAACcTTGCCCGGTTGCTCTTTCTCTATCTTCCCTTTTGGCTTTGCTATCC
111	D1	tTATGCAACAGGGAAtTTGCCCGGTTGCTCTTTCTCTATCTTCCCTTTGCTTTGCTGTC
112	US6	CTATGCAACAGGGAACcTTGCCCGGTTGCTCTTTCTCTATCTTCCCTTTGCTTTGCTGTC
113	P10	CTATGCAACAGGGAAtcTGCCCGGTTGCTCTTTCTCTATCTTCCCTTTGCTTTGCTGTC
114	DK1	CTAGCAACAGGGAAtTTGCCCGGTTGCTCTTTCTCTATCTTCCCTTTGCTCTGtTGTCC
115	T10	CTATGCAACAGGGAAtTTGCCCGGTTGCTCTTTCTCTATCTTCCCTTTGCTCTGCTGTCT
116	SW2	CTATGCAACAGGGAAtcTGCCCGGTTGCTCTTTCTCTATCTTCCCTTTGCTCTGCTGTCC
122	HK4	CTATGCAACAGGGAAtTTGCCCGGTTGCTCTTTCTCTATCTTCCCTTTGCTCTGCTGTCC
109	SA10	CTATGCAACAGGGAAtTTGCCCGGTTGCTCTTTCTCTATCTTCCCTTTGCTCTGCTGTCC
110	S45	CTATGCAACAGGGAAtcTGCCCGGTTGCTCTTTCTCTATCTTCCCTTTGCTCTGCTGTCC
123	P8	CTATGCAACAGGGAAtCTGCCCTGGTTGCTCTTTCTCTATCTTCCCTTTGCTCTGCTGTCT
124	T3	tTAcGCAACAGGGAAtTTGCCCTGGTTGCTCTTTCTCTATCTTCCCTTTGCTCTGCTGTCC
120	HK3	CTATGCAACAGGGAAtTTAcCCCGGTTGCTCTTTCTCTATCTTCCCTTTGCTCTGCTGTCC
121	HK5	CTAcGCAACAGGGAAtaTAcCCCGGTTGCTCTTTCTCTATCTTCCCTTTGCTCTGCTGTCC
108	DR4	CTATGCAACAGGGAAtCTTCCCTGGTTGCTCTTTCTCTATCTTCCCTTTGCTCTGCTCTCT
104	US11	CTATGCAACAGGGAACcTTCCCTGGTTGCTCTTTCTCTATCTTCCCTTTGCTCTGCTCTCT
105	S14	CTATGCAACAGGGAACcTTCCCTGGTTGCTCTTTCTCTATCTTCCCTTTGCTCTGCTCTCT
106	SW1	CTATGCAACAGGGAACcTTCCCTGGTTGCTCTTTCTCTATCTTCCCTTTGCTCTGCTCTCT
107	S18	CTATGCAACAGGGAACcTTCCCTGGTTGCTCTTTCTCTATCTTCCCTTTGCTCTGCTCTCT
103	DK7	CTATGCAACAGGGAACcTTCCCTGGTTGCTCTTTCTCTATCTTCCCTTTGCTCTGCTCTCT
103-124	consensus	cTAtGCAACAGGGAAtcTgCCcGGTTGctCtTtTcTcTATCTTCCCTctTgGcttTgctTgTCC

NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF
THE ENVELOPE 1...

Bukh et al.

Appl. No.: 09/084,691 Atty Docket: NIH240.1CPDV1
REPLACEMENT SHEET

FIGURE 6C-10

SEQ ID NO:	ISOLATE	
119	S9	550 TGTTTGACCATCCAGCTTCCGCT
117	IND3	550 TGTTTGACCATCCAGCTTCCGCT
118	IND8	550 TGTTTGACCATCCAGCTTCCGCT
111	D1	550 TGTTTGACCATCCAGCTTCCGCT
112	US6	550 TGTTTGACCATCCAGCTTCCGCT
113	P10	550 TGcctGACCATCCAGCgTCCGCT
114	DK1	550 TGttTGACCATCCAGCTTCCGCC
115	T10	550 TGCTTGACCATCCAGCTTCCGCT
116	SW2	550 TGCTTGACCATCCAGCTTCCGCT
122	HK4	550 TGTTTGACCATCCAGCTTCCGCT
109	SA10	550 TGTTTaACCATCCAGCTTCCGCT
110	S45	550 TGctTGACCATCCAGCTTCCGCT
123	P8	550 TGctTGACCATCCAGCTTCCGCT
124	T3	550 TGCTTGACCATCCAGCTTCCGCT
120	HK3	550 TGCTTGACCATCCAGCTTCCGCT
121	HK5	550 TGtcTGACCATCCAGCTTCCGCT
108	DR4	550 TGctTGACCGTGCCCGCaTcgGCC
104	US11	550 TGCCTGACTGTGCCCGCTTCAGCC
105	S14	550 TGCCTGACTGTGCCCGCTTCAGCC
106	SW1	550 TGCCTGACaGTGCCCGCGTCAGCC
107	S18	550 TGctTGACTGTGCCCGCGTCAGCT
103	DK7	550 TGcctGACcGTGCCCGCGctTcgGCC
103-124	consensus	TGttTgACcatcCCaGctTccGct

NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF
THE ENVELOPE 1...

Bukh et al.

Appl. No.: 09/084,691 Atty Docket: NIH240.1CPDV1
REPLACEMENT SHEET

FIGURE 6D-1

SEQ ID NO:	ISOLATE	
128	T2	1 ATGAGCACAATTCCTAAACCTCAAGAAAAACCAAGAAAAACACTAACCGTCGCCCCACAAG
125	T4	1 ATGAGCACAATTCCTAAACCTCAAGAAAAACCAAGAAAAACACTAACCGTCGCCCCACAAG
126	US10	1 ATGAGCACAATTCCTAAACCTCAAGAAAAACCAAGAAAAACACTAACCGTCGCCCCACAAG
127	T9	1 ATGAGCACAATTCCTAAACCTCAAGAAAAACCAAGAAAAACACTAACCGTCGCCCCACAAG
125-128	consensus	ATGAGCACAATTCCTAAACCTCAAGAAAAACCAAGAAAAACACTAACCGTCGCCCCACAAG
128	T2	62 ACGTTAAGTTCCGGGGCGGGCCAGATCGTTGGCGGAGTATCTTGCTGCCGCGCAGGGG
125	T4	62 ACGTTAAGTTCCGGGGCGGGCCAGATCGTTGGCGGAGTATCTTGCTGCCGCGCAGGGG
126	US10	62 ACGTTAAGTTCCGGGGCGGGCCAGATCGTTGGCGGAGTATCTTGCTGCCGCGCAGGGG
127	T9	62 ACGTTAAGTTCCGGGGCGGGCCAGATCGTTGGCGGAGTATCTTGCTGCCGCGCAGGGG
125-128	consensus	ACGTTAAGTTCCGGGGCGGGCCAGATCGTTGGCGGAGTATCTTGCTGCCGCGCAGGGG
128	T2	123 CCCAGGTTGGGTGTGCGCGCGACAAGGAAGACTTCGGAGCGGTCCCAGCCCTCGTGGaAGG
125	T4	123 CCCAGGTTGGGTGTGCGCGCGACAAGGAAGACTTCGGAGCGGTCCCAGCCCTCGTGGAGG
126	US10	123 CCCAGGTTGGGTGTGCGCGCGACAAGGAAGACTTCGGAGCGGTCCCAGCCCTCGTGGAGG
127	T9	123 CCCTAGGTTGGGTGTGCGCGCGACAAGGAAGACTTCGGAGCGGTCCCAGCCCTCGTGGAGG
125-128	consensus	CCCAGGTTGGGTGTGCGCGCGACAAGGAAGACTTCGGAGCGGTCCCAGCCCTCGTGGAGG
128	T2	184 CGCCAGCCCCATCCCTAAAGATCGGCGCTCCACTGGCAAGTCTCTGGGGAACCAAGGATACC
125	T4	184 CGCCAGCCCCATCCCTAAAGATCGGCGCTCCACTGGCAAGTCTCTGGGGAACCAAGGATACC
126	US10	184 CGCCAGCCCCATCCCTAAAGATCGGCGCTCCACTGGCAAGTCTCTGGGGAACCAAGGATACC
127	T9	184 CGCCAGCCCCATCCCTAAAGATCGGCGCTCCACTGGCAAGTCTCTGGGGAACCAAGGATACC
125-128	consensus	CGCCAGCCCCATCCCTAAAGATCGGCGCTCCACTGGCAAGTCTCTGGGGAACCAAGGATACC

FIGURE 6D-2

SEQ ID NO:	ISOLATE	
128	T2	245 CCTGGCCCCCTGTATGGGAATGAGGGCTTCGGCTGGGCAGGATGGCTCCTGTCCCCCGAGG
125	T4	245 CCTGGCCCCCTGTATGGGAATGAGGGCTTCGGCTGGGCAGGATGGCTCCTGTCCCCCGAGG
126	US10	245 CTTGGCCCCCTATATGGGAATGAGGGCTTCGGCTGGGCAGGATGGCTCCTGTCCCCCGAGG
127	T9	245 CcTGGCCCTCTATATGGGAATGAGGGCTTCGGCTGGGCAGGATGGCTCCTGTCCCCCGAGG
125-128	consensus	CcTGGCCcCT-TATGGGAATGAGGGaCTCGGCTGGGCaGGATGGCTCCTGTCCCCCGAGG
SEQ ID NO:	ISOLATE	
128	T2	306 TTCTCGTCCCTCTTGGGGCCCCAATGACCCCGGCATAGGTGCGCAATGTGGGTAAaGTC
125	T4	306 TTCCCGTCCCTCcTGGGGCCCCAATGACCCCGGCATAGGTGCGCAACGTGGGTAAaGTC
126	US10	306 TTCCCGTCCCTCTTGGGGCCCCCacTGATCCCCCGCATAGGTGCGCAACGTGGGTAAaGTC
127	T9	306 TTCCCGTCCCTCTTGGGGCCCCCagTGACCCCGGCATAGGTGCGCAACGTGGGTAAaGTC
125-128	consensus	TTCCcCGTCCCTCTTGGGGCCCCCaaTGAcCCCCCGCATAGGTGCGGCAAcGTGGGTAAaGTC
SEQ ID NO:	ISOLATE	
128	T2	367 ATCGATACCCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACaTCCCCGTCGTAGGGCGcCC
125	T4	367 ATCGATACCCCTAACGTGCaGCCTTGCCGACCTCATGGGGTACgTCCCCGTCGTAGGGCGcCC
126	US10	367 ATCGATACCCCTAACGTGCGGCTTTGCCGACCTCATGGGaTACATCCCCGTCGTgGGCGctC
127	T9	367 ATCGATACCCCTAACGTGCGGCTTTGCCGACCTCATGGGgTACATCCCCGTCGTaGGCGccC
125-128	consensus	ATCGATACCCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACaTCCCCGTCGTaGGCGccc
SEQ ID NO:	ISOLATE	
128	T2	428 CGcTtGGTGGTGTGCCAGAGCTCTtGGCATGGCGTCAGAGTCCTGGAGACGGaGTTAA
125	T4	428 CGtTgGGTGGCGTGCcCAGAGCTCTCGCGCATGGCGTCAGAGTCCTGGAGACCGGGTTAA
126	US10	428 CGCTTGGTGGCGTGCcCAGAGCTCTCGCGCATGGCGTCAGgGTCTCTGGAGACCGGGTTAA
127	T9	428 CGCTTGGTGGCGTtGCCAGAGCTCTCGCGCaCGCGTCAGaGTCTCTGGAGACCGGGTTAA
125-128	consensus	CGcTtGGTGGcGTcGCCAGAGCTCTcGGCGCaTGGCGTCAGaGTCTCTGGAGACGGgGTTAA

FIGURE 6D-3

SEQ ID NO:	ISOLATE	
128	T2	489 TTATGCAACAGGtAACTTACCcGGTTGCTCCTTTTCTATcTTCTTGCTaGCCCTgCTGTCC
125	T4	489 TTATGCAACAGGAACTTACCtGGTTGCTCCTTTTCTATcTTCTTGCTGGCCCTACTGTCC
126	US10	489 TTATGCAACAGGAACTTACCcGGTTGCTCCTTTTCTATcTTCTTGCTGGCCCTACTGTCC
127	T9	489 TTATGCAACAGGAAcTACCtGGTTGCTcTTTTCTATcTTCTTGCTGGCCcTACTGTCC
125-128	consensus	TTATGCAACAGGgAAcTACC - GGTTGCTCcTTTTCTATcTTCTTGCTgGCCcTaCTGTCC
SEQ ID NO:	ISOLATE	
128	T2	550 TGCATCAcAtATTCCgGtTtCaGCT
125	T4	550 TGCATCACCAATTCCAGTCTCcGCT
126	US10	550 TGCATCACCAATTCCAGTCTCTGCT
127	T9	550 TGCATCACCAcTCCGgcCTCTGCT
125-128	consensus	TGCATCACcAtTCC-GtcTctGCT

FIGURE 6E-1

SEQ ID NO:	ISOLATE	
131	DK11	1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAGAAATACAAACCGCGCCACAGG
132	SW3	1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAGAAATACAAACCGCGCCACAGG
133	DK8	1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAGAAATACAAACCGCGCCACAGG
129	T8	1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAGAAATACAAACCGCGCCACAGG
130	US1	1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAGAAATACAAACCGCGCCACAGG
129-133	consensus	ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAGAAATACAAACCGCGCCACAGG
SEQ ID NO:	ISOLATE	
131	DK11	62 ACGTTAAGTTCCCGGTGGCGGCCAGATCGTTGGCGGAGTTTACTTGTGCCGCGCAGGGG
132	SW3	62 ACGTTAAGTTCCCGGTGGCGGCCAGATCGTTGGCGGAGTTTACTTGTGCCGCGCAGGGG
133	DK8	62 ACGTTAAGTTCCCGGTGGCGGCCAGATCGTTGGCGGAGTTTACTTGTGCCGCGCAGGGG
129	T8	62 ACGTTAAGTTCCCGGTGGCGGCCAGATCGTTGGCGGAGTTTACTTGTGCCGCGCAGGGG
130	US1	62 ACGTTAAGTTCCCGGTGGCGGCCAGATCGTTGGCGGAGTTTACTTGTGCCGCGCAGGGG
129-133	consensus	ACGTTAAGTTCCCGGTGGCGGCCAGATCGTTGGCGGAGTTTACTTGTGCCGCGCAGGGG
SEQ ID NO:	ISOLATE	
131	DK11	123 CCCAGGTTGGGTGTGCGCaCGACAAGGAAGACTTCGAGCGATCCCAGCCGCGTGGGAGA
132	SW3	123 CCCAGGTTGGGTGTGCGCGCGACAAGGAAGACTTCGAGCGATCCCAGCCGCGTGGGAGA
133	DK8	123 CCCAGGTTGGGTGTGCGCGCGACAAGGAAGCTTCGAGCGATCCCAGCCGCGTGGGAGg
129	T8	123 CCCTAGGTTGGGTGTGCGCGCGACAAGGAAGACTTCGAGCGATCCCAGCCGCGTGGGAGA
130	US1	123 CCCAGGTTGGGTGTGCGCGCGACAAGGAAGACTTCGAGCGATCCCAGCCGCGTGGGAGA
129-133	consensus	CCCcAGGTTGGGTGTGCGGcCGACAAGGAAGaCTTCGAGCGATCCCAGCCGCGTGGGAGa

FIGURE 6E-2

SEQ ID NO:	ISOLATE	
131	DK11	184 CGCCAGCCCATCCGAAAGATCGGCGCTCCACCGCAAGcCCTGGGAAAGCCAGGATATC
132	SW3	184 CGCCAGCCCATCCGAAAGATCGGCGCTCCACCGCAAGTCTTGGGAAAGCCAGGATATC
133	DK8	184 CGCCAGCCCATCCGAAAGATCGGCGCTCCACCGCAAGTCTTGGGAAAGCCgGGATATC
129	T8	184 CGCCAGCCCATCCGAAAGATCGGCGCTCCACCGCAAGTCTTGGGAAAGCCAGGATATC
130	US1	184 CGCCAGCCCATCCGAAAGATCGGCGCTCCACCGCAAGTCTTGGGAAAGCCAGGATATC
129-133	consensus	CGCCAGCCCATCCGAAAGATCGGCGCTCCACCGCAAGTCTTGGGAAAGCCAGGATATC
SEQ ID NO:	ISOLATE	
131	DK11	245 CTTGGCCCCGTGTATGGAAACGAGGGCTGCGGCTGGGCAGGTTGGCTCCTGTCCCCCGCGG
132	SW3	245 CTTGGCCCCGTGTATGGAAACGAGGGCTGCGGCTGGGCAGGTTGGCTCCTGTCCCCCGCGG
133	DK8	245 CTTGGCCCCGTGTATGGAAACGAGGGCTGCGGCTGGGCAGGTTGGCTCCTGTCCCCCGCGG
129	T8	245 CTTGGCCTCTtTACGGAACGAGGGCTGCGGtTGGGCAGGTTGGCTCCTGTCCCCCGCGG
130	US1	245 CTTGGCCTCTgTACGGAACGAGGGCTGCGGcTGGGCAGGTTGGCTCCTGTCCCCCGCGG
129-133	consensus	CTTGGCCCCGTGTATGGAAACGAGGGCTGCGGcTGGGCAGGTTGGCTCCTGTCCCCCGCGG
SEQ ID NO:	ISOLATE	
131	DK11	306 GTCTCATCCTAATTTGGGGCCCCACTGACCCCCGGCATAaATCACGCAATTTGGtAAAGTC
132	SW3	306 GTCTCATCCTAATTTGGGGCCCCACTGACCCCCGGCATAATTCAGCAATTTGGGCAAGTC
133	DK8	306 GTCTCGTCTACTTTGGGGCCCCACTGACCCCCGGCATAAGATCACGCAATTTGGGCAAGTC
129	T8	306 GTCTCGTCTACTTTGGGGCCCCACTGACCCCCGGCATAAGATCACGTAATTTGGGCAAGTC
130	US1	306 GTCTCGTCTACTTTGGGGCCCCACTGACCCCCGGCACAAGATCACGTAACTTGGGCAagGTC
129-133	consensus	GTCTCGTCTACTTTGGGGCCCCACTGACCCCCGGCAtAgATCACGCAATTTGGGCAaaGTC

FIGURE 6E-3

SEQ ID NO:	ISOLATE	
131	DK11	367 ATCGACACCATTAAGTGTGGTTTGGCCGACCTCATGGGTACATCCCTGTGCTGGCGCCC
132	SW3	367 ATCGACACCATTAAGTGTGGTTTGGCCGACCTCATGGGTACATCCCTGTGCTGGCGCCC
133	DK8	367 ATCGACACCATTAAGTGTGGTTTGGCCGACCTCATGGGTACATCCCTGTGCTGGCGCCC
129	T8	367 ATCGATACCATTAACaTGTGGTTTGGCCGACCTCATGGGTACATCCCTGTGCTGGCGCCC
130	US1	367 ATCGATACCATTAACgTGTGGTTTGGCCGACCTCATGGGTACATCCCTGTGCTGGCGCCC
129-133	consensus	ATCGACACCATTAACgTGTGGTTTGGCCGACCTCATGGGTACATCCCTGTGCTGGCGCCC
SEQ ID NO:	ISOLATE	
131	DK11	428 CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTAGAGTCTTGAAGACGGGATAAA
132	SW3	428 CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTAGAGTCTTGAAGACGGGATAAA
133	DK8	428 CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTAGAGTCTTGAAGACGGGATAAA
129	T8	428 CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTAGAGTCTTGAAGACGGGATAAA
130	US1	428 CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTAGAGTCTTGAAGACGGGATAAA
129-133	consensus	CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTAGAGTCTTGAAGACGGGATAAA
SEQ ID NO:	ISOLATE	
131	DK11	489 TTACGCAACAGGGAATCTGCCTGGTTGCTCTTTTCTATCTTCTTACTTGTCTCTGTCTCa
132	SW3	489 TTACGCAACAGGGAATCTGCCTGGTTGCTCTTTTCTATCTTCTTACTTGTCTCTGTCTCG
133	DK8	489 TTACGCAACAGGGAATTTGCCTGGTTGCTCTTTTCTATCTTCTTGTCTCTCTGTCTCG
129	T8	489 cTAcGCAACAGGGAATTTGCCTGGTTGCTCTTTTCTATCTTCTTGTCTCTCTGTCTCa
130	US1	489 tTAcGCAACAGGGAATcTGcCTGGTTGCTCcTTTTCTATCTTCTTaCTTGTCTCTCTGTCTCG
129-133	consensus	tTAcGCAACAGGGAATcTGcCTGGTTGCTCtTTTTCTATCTTCTTaCTTGTCTCTCTGTCTCG

NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF
THE ENVELOPE 1...

Bukh et al.

Appl. No.: 09/084,691 Atty Docket: NIH240.1CPDV1
REPLACEMENT SHEET

FIGURE 6E-4

<u>SEQ ID NO:</u>	<u>ISOLATE</u>	
131	DK11	550 TGCTgCACAGTGCCAGTGTCTGCG
132	SW3	550 TGCTtCACAGTGCCAGTGTCTGCG
133	DK8	550 TGCTgCACAGTGCCAGTGTCTGCG
129	T8	550 TGCTtCACAGTGCCAGTGTCTGCA
130	US1	550 TGCgcCACgGTGCCgGTGTCTGCA
129-133	consensus	TGct - CACaGTGCCaGTGTCTGcg

FIGURE 6F-1

SEQ ID NO:	ISOLATE	
131	DK11	1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAAGAAATACAAACCGCGCCACAGG
132	SW3	1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAAGAAATACAAACCGCGCCACAGG
133	DK8	1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAAGAAATACAAACCGCGCCACAGG
129	T8C	1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAAGAAATACAAACCGCGCCACAGG
130	US1	1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAAGAAATACAAACCGCGCCACAGG
125	T4	1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAAGAAATACAAACCGCGCCACAGG
126	US10	1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAAGAAATACAAACCGCGCCACAGG
127	T9	1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAAGAAATACAAACCGCGCCACAGG
128	T2	1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAAGAAATACAAACCGCGCCACAGG
134	S83	1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAAGAAATACAAACCGCGCCACAGG
125-134	consensus	ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAAGAAATACAAACCGCGCCACAGG
131	DK11	62 ACGTTAAGTTCCCGGTGGCGGCCAGATCGTTGGCGGAGTTTACTTGTGCGCGCAGGGG
132	SW3	62 ACGTTAAGTTCCCGGTGGCGGCCAGATCGTTGGCGGAGTTTACTTGTGCGCGCAGGGG
133	DK8	62 ACGTTAAGTTCCCGGTGGCGGCCAGATCGTTGGCGGAGTTTACTTGTGCGCGCAGGGG
129	T8	62 ACGTCAAGTTCCCGGTGGCGGCCAGATCGTTGGCGGAGTTTACTTGTGCGCGCAGGGG
130	US1	62 ACGTCAAGTTCCCGGTGGCGGCCAGATCGTTGGCGGAGTTTACTTGTGCGCGCAGGGG
125	T4	62 ACGTTAAGTTCCCGGTGGCGGCCAGATCGTTGGCGGAGTTTACTTGTGCGCGCAGGGG
126	US10	62 ACGTTAAGTTCCCGGTGGCGGCCAGATCGTTGGCGGAGTTTACTTGTGCGCGCAGGGG
127	T9	62 ACGTTAAGTTCCCGGTGGCGGCCAGATCGTTGGCGGAGTTTACTTGTGCGCGCAGGGG
128	T2	62 ACGTTAAGTTCCCGGTGGCGGCCAGATCGTTGGCGGAGTTTACTTGTGCGCGCAGGGG
134	S83	62 ACGTCAAGTTCCCGGTGGCGGCCAGATCGTTGGCGGAGTTTACTTGTGCGCGCAGGGG
125-134	consensus	ACGTTAAGTTCCCGGG-GGcGGcCAGATCGTTGGCGGAGT-TACTTgcTGCCGCGCAGGGG

FIGURE 6F-2

SEQ ID NO:	ISOLATE	
131	DK11	123 CCCAGGTTGGTGTGCGCaCGACAAGGAAGACTTCCGAGCGATCCAGCCGCGTGGGAGA
132	SW3	123 CCCAGGTTGGTGTGCGCGGACAAGGAAGACTTCCGAGCGATCCAGCCGCGTGGGAGA
133	DK8	123 CCCAGGTTGGTGTGCGCGGACAAGGAAGTCTTCCGAGCGATCCAGCCGCGTGGGAGg
129	T8	123 CCctAGGTTGGTGTGCGCGGACAAGGAAGACTTCCGAGCGATCCAGCCGCGTGGGAGA
130	US1	123 CCCAGGTTGGTGTGCGCGGACAAGGAAGACTTCCGAGCGATCCAGCCGCGTGGGAGA
125	T4	123 CCCAGGTTGGTGTGCGCGGACAAGGAAGACTTCCGAGCGATCCAGCCACGTGGGAGg
126	US10	123 CCCAGGTTGGTGTGCGCGGACAAGGAAGACTTCCGAGCGGTCCAGGCCACGTGGGAGg
127	T9	123 CCctAGGTTGGTGTGCGCaCGACAAGGAAGACTTCCGAGCGGTCCAGGCCACGTGGGAGg
128	T2	123 CCCcAGGTTGGTGTGCGCGGACAAGGAAGACTTCCGAGCGGTCCAGGCctCGTGGAAGg
134	S83	123 CCCgAGaTTGGTGTGCGCGGACgAGGAaAaACTTCCGAaCGGTCCAGGCCaCGTGgGgAGg
125-134	consensus	CCCcAGgTTGGTGTGCGCGCGACaAGGAAGaCTTCCgAGCGaTCCcAGCCgCGTGgGgAGg
131	DK11	184 CGCCAGCCCCATCCCGAAAGATCGGCGCTCCACCGGCAAGcCCTGGGAAAGCCAGGATATC
132	SW3	184 CGCCAGCCCCATCCCGAAAGATCGGCGCTCCACCGGCAAGTCTTGGGAAAGCCAGGATATC
133	DK8	184 CGCCAGCCCCATCCCGAAAGATCGGCGCTCCACCGGCAAGTCTTGGGAAaACCGGATATC
129	T8	184 CGCCAGCCCCATCCCGAAAGATCGGCGCTCCACCGGCAAGTCTTGGGAAaACCGGATATC
130	US1	184 CGCCAGCCCCATCCCGAAAGATCGGCGCTCCACCGGCAAGTCTTGGGAAaACCGGATATC
125	T4	184 CGCCAGCCCCATCCCGAAAGATCGGCGCTCCACTGGCAAGTCTTGGGAAaACCGGATATC
126	US10	184 CGCCAGCCCCATCCCGAAAGATCGGCGCcCCACTGGCAAGTCTTGGGAAaACCGGATATC
127	T9	184 CGCCAGCCCCATCCCGAAAGATCGGCGCTCCACTGGCAAGTCTTGGGAAaACCGGATATC
128	T2	184 CGCCAGCCCCATCCCTAAAGATCGGCGCTCCACTGGCAAGTCTTGGGAAaACCGGATATC
134	S83	184 CGCCAGCCCCATCCCTAAAGATCGGCGCaCCACTGGCAAGTCTTGGGAAgGCCAGGATATC
125-134	consensus	CGCCAGCCCCATCCCGAAAGATCGGCGCTCCAC-GGCAAGTCTTGGGAAaACCGGATATC

FIGURE 6F-3

SEQ ID NO:	ISOLATE
131	DK11
132	SW3
133	DK8
129	T8
130	US1
125	T4
126	US10
127	T9
128	T2
134	S83
125-134	consensus
245	CTTGGCCCCCTGATGGAACGAGGGCTGCGGCTGGGAGGTTGGCTCCTGTCCTCCCCCGCGG
245	CTTGGCCCCCTGATGGAACGAGGGCTGCGGCTGGGAGGTTGGCTCCTGTCCTCCCCCGCGG
245	CTTGGCCCCCTGATGGAACGAGGGCTGCGGCTGGGAGGTTGGCTCCTGTCCTCCCCCGCGG
245	CTTGGCCCTCTTACGGAACGAGGGCTGCGGCTGGGAGGTTGGCTCCTGTCCTCCCCCGCGG
245	CTTGGCCCTCTGACGGAACGAGGGCTGCGGCTGGGAGGTTGGCTCCTGTCCTCCCCCGCGG
245	CcTGGCCCCCTGATGGGAATGAGGGACTCGGCTGGGAGGATGGCTCCTGTCCTCCCCCGAGG
245	CtTGGCCCCCTATATGGGAATGAGGGACTCGGCTGGGAGGATGGCTCCTGTCCTCCCCCGAGG
245	CCTGGCCCTCTATATGGGAATGAGGGACTCGGCTGGGCGGATGGCTCCTGTCCTCCCCCGAGG
245	CCTGGCCCCCTGATGGGAATGAGGGCTCGGCTGGGAGGATGGCTCCTGTCCTCCCCCGAGG
245	CtTGGCCCCCTGATGGGAATGAGGGCTCGGCTGGGAGGgTGGCTCCTGTCCTCCCCCGCGG
	CtTGGCCcCTgTAtGG-AA-GAGGGc--CGGcTGGGCaGGtTGGTCCTGTCCTCCCCCGCGG
306	GTCTCATCCTAATTGGGGCCCCCACTGACCCCCGGCATAAATCACGCAATTTGGGTAAAGTC
306	GTCTCATCCTAATTGGGGCCCCCACTGACCCCCGGCATAGATCACGCAATTTGGGCAAGTC
306	GTCTCGTCCTACTTGGGGCCCCCACTGACCCCCGGCATAGATCACGCAATTTGGGCAAGTC
306	GTCTCGTCCTACTTGGGGCCCCCACTGACCCCCGGCATAGATCACGTAATTTGGGCAAGTC
306	GTCTCGTCCTACTTGGGGCCCCCACTGACCCCCGGCAcAGATCACGTAACCTTGGGCAAGTC
306	TTCCCGTCCCTCcTGGGGCCCCCAaTGACCCCCGGCATAGGTCGGCAACCGTGGGTAAAGTC
306	TTCCCGTCCCTCTTGGGGCCCCCAcTGATCCCCGGCATAGGTCGGCAACCGTGGGTAAAGTC
306	TTCCCGTCCCTCTTGGGGCCCCCAgTGACCCCCGGCATAGGTCGGCAACCGTGGGTAAAGTC
306	TTCTCGTCCTCTTGGGGCCCCCAaTGACCCCCGGCATAGGTCGGCAaATGTGGGTAAaGTC
306	TTCTCGcCCTTCaTGGGGCCCCCAccGACCCCCGGCATaaTCGGCGCAActTGGGTAAgTc
125-134	-TcTcGtCct-ctTGGGGCCCCCAcTGAcCCCCGGCAtAgaTc-CGcAA-tTGGGTAA-GTC
SEQ ID NO:	ISOLATE
131	DK11
132	SW3
133	DK8
129	T8
130	US1
125	T4
126	US10
127	T9
128	T2
134	S83
125-134	consensus

FIGURE 6F-4

SEQ ID NO:	ISOLATE	
131	DK11	367 ATCGACACCATTAACGTGTGGTTTTCGCCGACCTCATGGGGTACATCCCTGTCTGTCGGCGCCC
132	SW3	367 ATCGACACCATTAACGTGTGGTTTTCGCCGACCTCATGGGGTACATCCCTGTCTGTCGGCGCCC
133	DK8	367 ATCGACACCATTAACGTGTGGTTTTCGCCGACCTCATGGGGTACATCCCTGTCTGTCGGCGCCC
129	T8	367 ATCGATACCATTAACGTGTGGTTTTCGCCGACCTCATGGGGTACATCCCTGTCTGTCGGCGCCC
130	US1	367 ATCGATACCATTAACGTGTGGTTTTCGCCGACCTCATGGGGTACATCCCTGTCTGTCGGCGCCC
125	T4	367 ATCGATACCATTAACGTGTGGTTTTCGCCGACCTCATGGGGTACATCCCTGTCTGTCGGCGCCC
126	US10	367 ATCGATACCATTAACGTGTGGTTTTCGCCGACCTCATGGGGTACATCCCTGTCTGTCGGCGCCC
127	T9	367 ATCGATACCATTAACGTGTGGTTTTCGCCGACCTCATGGGGTACATCCCTGTCTGTCGGCGCCC
128	T2	367 ATCGATACCATTAACGTGTGGTTTTCGCCGACCTCATGGGGTACATCCCTGTCTGTCGGCGCCC
134	S83	367 ATCGATACCATTAACGTGTGGTTTTCGCCGACCTCATGGGGTACATCCCTGTCTGTCGGCGCCC
125-134	consensus	ATCGATACC-T-ACGTG-ggttTTGCCGACCTCATGGGGTACaTcCC-GTCGTtGGCGccc
SEQ ID NO:	ISOLATE	
131	DK11	428 CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACCGGTGTTAGAGTCTCTGGAAGACGGGATAAA
132	SW3	428 CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACCGGTGTTAGAGTCTCTGGAAGACGGGATAAA
133	DK8	428 CGGTtGGAGGCGTCGCCAGAGCTCTGGCACACCGGTGTTAGGTCCTTGAAGACGGGATAAA
129	T8	428 CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACCGGTGTTAGGTCCTTGAAGACGGGATAAA
130	US1	428 CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACCGGTGTTAGGTCCTTGAAGACGGGATAAA
125	T4	428 CgtTgGTGGCGTCGCCAGAGCTCTCGCGCATGGCGTGAGaGTCTCTGGAGGACGGGGTTAA
126	US10	428 CGCTTGTGGCGTCGCCAGAGCTCTCGCGCATGGCGTGAGgGTCTCTGGAGGACGGGGTTAA
127	T9	428 CGCTTGTGGCGTtGCCAGAGCTCTCGCGCaCGGCGTGAGAGTCTCTGGAGGACGGGGTTAA
128	T2	428 CGCTTGTGTGgtGTcGCCAGAGCTCTtCGGCATGGCGTGAGAGTCTCTGGAGGACGGaGTTAA
134	S83	428 CcgTTGGcGGcGTTtGCCAGAGCcTcGccCATGGgGTGAGgGTTtCTGGAGGACGGgaTaaa
125-134	consensus	CggTtGGaGGcGTcGCCAGAGCtCTgCaCA-GgtGT-AG-GTcCTGGA-GACGGgaTaaa

FIGURE 6F-5

SEQ ID NO:	ISOLATE	
131	DK11	489 TTACGCAACAGGGAATCTGCCTGGTTGCTCTTTTCTATCTTACTTGTCTCTTGTCTCa
132	SW3	489 TTACGCAACAGGGAATCTGCCTGGTTGCTCTTTTCTATCTTACTTGTCTCTTGTCTCG
133	DK8	489 TTACGCAACAGGGAATTTGCCTGGTTGCTCTTTTCTATCTTACTTGTCTCTTGTCTCG
129	T8	489 cTAtGCAACAGGGAATTTGCCTGGTTGCTCTTTTCTATCTTACTTGTCTCTTGTCTCa
130	US1	489 TTACGCAACAGGGAATcTGCTGGTTGCTCTTTTCTATCTTACTTGTCTCTTGTCTCG
125	T4	489 TTATGCAACAGGGAACCTTACCTGGTTGCTCTTTTCTATCTTACTTGTCTCTTGTCTCC
126	US10	489 TTATGCAACAGGGAACCTTACcGGTTGCTCTTTTCTATCTTACTTGTCTGGCCCTACTGTCC
127	T9	489 TTATGCAACAGGGAACcTACcTGGTTGCTCTTTTCTATCTTACTTGTCTGGCCCTACTGTCC
128	T2	489 TTATGCAACAGGtAACTTACCCGGTTGCTCTTTTCTATCTTACTTGTCTaGCCCTgCTGTCC
134	S83	489 TTATGCAACgGGgAAATTgCCCGTTGCTCTTTcTCTATCTTctTctTgGCCCTctTGTCTc
125-134	consensus	tTAtGCAACaGGgAAAttTgCctGGTTGCTCTTTtTCTATcTTctTgcTtGC-cTtctGTCTCc
550	DK11	TGCTgCACAGTGCCAGTGTCTGGG
550	SW3	TGCTtCACAGTGCCAGTGTCTGGG
550	DK8	TGCTgCACAGTGCCAGTGTCTGGG
550	T8	TGCTtCACAGTGCCAGTGTCTGCA
550	US1	TGcGcCACgGTGCCgGTCTGCA
550	T4	TGCATCACCAATCCAGTCTCcGCT
550	US10	TGCATCACCAATCCAGTCTCTGCT
550	T9	TGCATCACCAcTCCGGcCTCTGCT
550	T2	TGCATCACTATTCGGGTTTCaGCT
550	S83	TGCATCtCTgTgCCaGTTTCcGcc
125-134	consensus	TGCatCaCagtGCCaGtGTctGct

FIGURE 6G-1

SEQ ID NO:	ISOLATE	
138	DK12	1 ATGAGCACACTTCCTAAACCTCAAGAAGAAAAACCAAGAAAAACCAATCCGTGCGCCACAGG
135	HK10	1 ATGAGCACACTTCCTAAACCTCAAGAAGAAAAACCAAGAAAAACCAATCCGTGCGCCACAGG
136	S52	1 ATGAGCACACTTCCTAAACCTCAAGAAGAAAAACCAAGAAAAACCAATCCGTGCGCCACAGG
137	S2	1 ATGAGCACACTTCCTAAACCTCAAGAAGAAAAACCAAGAAAAACCAATCCGTGCGCCACAGG
135-138	consensus	ATGAGCACACTTCCTAAACCTCAAGAAGAAAAACCAAGAAAAACCAATCCGTGCGCCACAGG
SEQ ID NO:	ISOLATE	
138	DK12	62 ACGTCAAGTTCCCGGTGGCGGACAGATCGTTGGTGGAGTATACGTGTGCCGCGCAGGGG
135	HK10	62 ACGTCAAGTTCCCGGTGGCGGACAGATCGTTGGTGGAGTATACGTGTGCCGCGCAGGGG
136	S52	62 ACGTCAAGTTCCCGGTGGCGGACAGATCGTTGGTGGAGTATACGTGTGCCGCGCAGGGG
137	S2	62 ACGTCAAGTTCCCGGTGGCGGACAGATCGTTGGTGGAGTATACGTGTGCCGCGCAGGGG
135-138	consensus	ACGTCAAGTTCCCGGTGGCGGACAGATCGTTGGTGGAGTATACGTGTGCCGCGCAGGGG
SEQ ID NO:	ISOLATE	
138	DK12	123 CCCACGATTGGGTGTGCGCGGACGCGTAAACTTCTGAACGGTcaCAGCCTCGCGGACGg
135	HK10	123 CCCACGATTGGGTGTGCGCGGACGCGTAAACTTCTGAACGGTcgCAGCCTCGCGGACGA
136	S52	123 CCCACGATTGGGTGTGCGCGGACGCGTAAACTTCTGAACGGTcACAGCCTCGCGGACGA
137	S2	123 CCCACGATTGGGTGTGCGCGGACGCGTAAACTTCTGAACGGTcACAGCCTCGCGGACGg
135-138	consensus	CCCACGATTGGGTGTGCGCGGACGCGTAAACTTCTGAACGGTcaCAGCCTCGCGGACG-
SEQ ID NO:	ISOLATE	
138	DK12	184 CGACAGCCTATCCCCAAGGCGGTGGAGCGAAGGCCGGTCTGGGCTCAGCCTGGGTACC
135	HK10	184 CGACAGCCTATCCCCAAGGCGGTGGAGCGAAGGCCGGTCTGGGCTCAGCCCGGGTACC
136	S52	184 CGACAGCCTATCCCCAAGGCGGTGGAGCGAAGGCCGGTCTGGGCTCAGCCCGGGTACC
137	S2	184 CGACAGCCTATCCCCAAGGCGGTGGAGCGAAGGCCGGTCTGGGCTCAGCCCGGGTACC
135-138	consensus	CGACAGCCTATCCCCAAGGCGGTGGAGCGAAGGCCGGTCTGGGCTCAGCCcGGGTACC

FIGURE 6G-2

SEQ ID NO:	ISOLATE	
138	DK12	245 CTTGGCCCCCTCTATGGTAACGAGGGCTGCGGGTGGGAGGgTGGCTCCTGTCCCCACGCGG
135	HK10	245 CTTGGCCCCCTCTATGGTAACGAGGGCTGCGGGTGGGAGGgTGGCTCCTGTCCCCACGCGG
136	S52	245 CTTGGCCCCCTCTATGGTAACGAGGGCTGCGGGTGGGAGGgTGGCTCCTGTCCCCACGCGG
137	S2	245 CTTGGCCCCCTCTATGGTAACGAGGGCTGCGGGTGGGAGGgTGGCTCCTGTCCCCACGCGG
135-138	consensus	CTTGGCCCCCTCTATGGTAACGAGGGCTGCGGGTGGGAGGgTGGCTCCTGTCCCCACGCGG
SEQ ID NO:	ISOLATE	
138	DK12	306 CTCCCGTCCATCTTGGGGCCCAACGACCCCCGGCGgaGGTCCCGCAATTGGGTAAGTC
135	HK10	306 CTCCCGTCCATCTTGGGGCCCAACGACCCCCGGCGgaGGTCCCGCAATTGGGTAAGTC
136	S52	306 CTCCCGTCCATCTTGGGGCCCAACGACCCCCGGCGgaGGTCCCGCAATTGGGTAAGTC
137	S2	306 CTCCCGTCCATCTTGGGGCCCAAAcGACCCCCGGCGgaGGTCCCGCAATTGGGTAAGTC
135-138	consensus	CTCCCGTCCATCTTGGGGCCCAACGACCCCCGGCGgaGGTCCCGCAATTGGGTAAGTC
SEQ ID NO:	ISOLATE	
138	DK12	367 ATCGATACCCCTcACGTGCGGATTcGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC
135	HK10	367 ATCGATACCCCTTACGTGCGGATTcGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC
136	S52	367 ATCGATACCCCTTACGTGCGGATTcGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC
137	S2	367 ATCGATACCCCTTACGTGCGGcTTGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC
135-138	consensus	ATCGATACCCCTcACGTGCGGgATTcGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC
SEQ ID NO:	ISOLATE	
138	DK12	428 CtGTAGGgGGCGTcGCAAGAGCCCTCGCGCATGGCGTAgGGGCCCTTGAAGACGGGATAAA
135	HK10	428 CCGTAGGAGGCGTcGCAAGAGCCCTCGCGCATGGCGTAgGGGCCCTTGAAGACGGGATAAA
136	S52	428 CCGTAGGAGGCGTcGCAAGAGCCCTCGCGCATGGCGTAgGGGCCCTTGAAGACGGGATAAA
137	S2	428 CCGTAGGAGGCGTcGCAAGAGCCCTCGCGCATGGCGTAgGGGCCCTTGAAGACGGGATAAA
135-138	consensus	CcGTAGGAGGCGTcGCAAGAGCCCTCGCGCATGGCGTAgGGGCCCTTGAAGACGGGATAAA

FIGURE 6G-3

SEQ ID NO:	ISOLATE	
138	DK12	489 TTTGCAACAGGAACTTGCCCGGTTGCTCCTTTCTATCTTCCTTCTTGCTCTGTTCTCT
135	HK10	489 TTTGCAACAGGAACTTGCCCGGTTGCTCCTTTCTATCTTCCTTCTTGCTCTGTTCTCT
136	S52	489 TTTTGCACACAGGAACTTGCCCGGTTGCTCCTTTCTATCTTCCTTCTTGCTCTGTTCTCC
137	S2	489 TTTTGCACACAGGAACTTGCCCGGTTGCTCCTTTCTATCTTCCTTCTTGCTCTGTTCTCT
135-138	consensus	TTT-GCAACAGGAACTTGCCCGGTTGCTCCTTTCTATCTTCCTTCTTGCTCTGTTCTCT
SEQ ID NO:	ISOLATE	
138	DK12	550 TGCCTAATTTCATCCAGCAGCTAGT
135	HK10	550 TGCCTAATTTCATCCAGCAGCTAGT
136	S52	550 TGCTTAGTTTCATCCTGCAGCTAGT
137	S2	550 TGCCTAATTTCATCCAGCAGCTAGT
135-138	consensus	TGCTTAATTTCATCCAGCAGCTAGT

FIGURE 6H-1

SEQ ID NO:	ISOLATE	
145	DK13	1 ATGAGCAGCAATCCTAAACCTCAAAGAAAAACCAAAACGTAACACCAACCGCGCGCCCaATGG
143	Z6	1 ATGAGCAGCAATCCTAAACCTCAAAGAAAAACCAAAACGTAACACCAACCGCGCGCCCaATGG
144	Z7	1 ATGAGCAGCAATCCTAAACCTCAAAGAAAAACCAAAACGTAACACCAACCGCGCGCCCaATGG
140	Z8	1 ATGAGCAGCAATCCTAAACCTCAAAGAAAAACCAAAACGTAACACCAACCGCGCGCCCaATGG
139	Z4	1 ATGAGCAGCAATCCTAAACCTCAAAGAAAAACCAAAACGTAACACCAACCGCGCGCCCaATGG
142	Z5	1 ATGAGCAGCAATCCTAAACCTCAAAGAAAAACCAAAACGTAACACCAACCGCGCGCCCaATGG
141	Z1	1 ATGAGCAGCAATCCTAAACCTCAAAGAAAAACCAAAACGTAACACCAACCGCGCGCCCaATGG
139-145	consensus	ATGAGCAGCAATCCTAAACCTCAAAGAAAAACCAAAACGTAACACCAACCGCGCGCCCaATGG
SEQ ID NO:	ISOLATE	
145	DK13	62 ACGTTAAAGTTCCCGGTGGCGCCAGATCGTTGGCGGAGTTTACTTTGTCGCGCAGGGG
143	Z6	62 ACGTTAAAGTTCCCGGTGGCGCCAGATCGTTGGCGGAGTTTACTTTGTCGCGCAGGGG
144	Z7	62 ACGTTAAAGTTCCCGGTGGCGCCAGATCGTTGGCGGAGTTTACTTTGTCGCGCAGGGG
140	Z8	62 ACGTTAAAGTTCCCGGTGGCGCCAGATCGTTGGCGGAGTTTACTTTGTCGCGCAGGGG
139	Z4	62 ACGTTAAAGTTCCCGGTGGCGCCAGATCGTTGGCGGAGTTTACTTTGTCGCGCAGGGG
142	Z5	62 ACGTTAAAGTTCCCGGTGGCGCCAGATCGTTGGCGGAGTTTACTTTGTCGCGCAGGGG
141	Z1	62 ACGTTAAAGTTCCCGGTGGCGCCAGATCGTTGGCGGAGTTTACTTTGTCGCGCAGGGG
139-145	consensus	ACGT-AAAGTTCCCGGGTGGCGCCAGATCGTTGGCGGAGTTTACTTTGTCGCGCAGGGG
SEQ ID NO:	ISOLATE	
145	DK13	123 CCCtAgATTGGGTGTGCGCGGACTAGGAAGACTTCGGAGCGGTGCGCAACCTCGTGGGAGG
143	Z6	123 CCCcAgTTGGGTGTGCGCGGACTAGGAAGACTTCGGAGCGGTGCGCAACCTCGTGGGAGA
144	Z7	123 CCCcAgTTGGGTGTGCGCaCACTAGGAAGACTTCGGAGCGGTGCGCAACCTCGTGGGAGA
140	Z8	123 CCCcAgTTGGGTGTGCGCGGACTCGGAAGACTTCGGAGCGGTGCGCAACCTCGTGGCAGG
139	Z4	123 CCCcAgTTGGGTGTGCGCGGACTCGGAAGACTTCGGAGCGGTGCGCAACCTCGTGGCAGG
142	Z5	123 CCCcAgTTGGGTGTGCGCGGACTCGGAAGACTTCGGAGCGGTGCGCAACCTCGcGGCAGG
141	Z1	123 CCCcGGTTGGGTGTGCGCGCagCTCGGAAGACTTCGGAGCGGTCaCAACCTCGtGGCAGG
139-145	consensus	CCCcAgTTGGGTGTGCGCGGcGagCTCGGAAGACTTCGGAGCGGTcGCAACCTCGtGGcAGG

FIGURE 6H-2

SEQ ID NO:	ISOLATE	
145	DK13	
143	Z6	184 CGCCAGCCTATCCCCAAGGCGCGcCaActcGAGGGtAGGTCTTGGGCTCAGCCTGGGTATC
144	Z7	184 CGCCAGCCTATCCCCAAGGCGCGTcGATCTGAGGGAAGGTCTTGGGCTCAGCCCGGTATC
140	Z8	184 CGTCAGCCTATCCCCAAGGCGCGTcGATCTGAGGGAAGGTCTTGGGCTCaaCCCCGGGTACC
139	Z4	184 CGTCAGCCTATCCCCAAGGCGCGTcGAGGGtAGGTCTTGGGCTCAGCCCGGGTACC
142	Z5	184 CGTCaAcCTATCCCCAAGGCGCGcCaGcCaGAGGGCAGATcCTGGGCGCAGCCCGGGTACC
141	Z1	184 CGTCAGCCTATCCCCAAGGCGCGcCGTcCGGTCCGAGGGCAGGTCTTGGGCTCAGCCCGGGTACC
139-145	consensus	CGtCAGcCTATCCCCAAGGCGCGtCggtccGAGGGcAGgTCCTGGGCTCAGcCCcGGGTACC
145	DK13	
143	Z6	245 CtTGGCCcCTTTACGGcCAATGAGGGcTGCGGGTGGCGGGATGGCTCCTGTCAcCCCCGTGG
144	Z7	245 CATGGcCTCTTTACGGTAATGAGGGtTGCGGGTGGCGGGATGGCTCCTGTCAcCCCCGTGG
140	Z8	245 CATGGcCTCTTTACGGTAACGAGGGtTGCGGGTGGCGGGATGGCTCCTGTCAcCCCCGTGG
139	Z4	245 CATGGcCTCTTTACGGTAATGAaGGCTGcGGGTGGCGAGGTGGCTCCTGTCTcCCCCCGGG
142	Z5	245 CTTGGCCcCTcTATGGCAATGAGGGCTGcGGGTGGCGAGGTGGCTCCTGTCTcCCCCCGGG
141	Z1	245 CTTGGCCcCTTTATGGCAATGAGGGCTGcGGGTGGCGAGGTGGCTCCTGTCTcCCCCCGGG
139-145	consensus	CtTGGCCcCTtTAcGGcCAATGAGGGcTGcGGGTGGGCaGG-TGGCTCcTGTC-CCcCGcGG
145	DK13	
143	Z6	306 CTCTCGgCCGTCTTGGGGcCCgAATGATCCCCGGCGgAGGTCCCGCAACTTGGGTAAAGTC
144	Z7	306 CTCTCGACCGTCTTGGGGtCCAAATGATCCCCGGCGAAGGTCCCGCAACTTGGGTAAAGTC
140	Z8	306 CTCTCGACCGTCTTGGGGCCCAATGATCCCCGGCGAAGGTCCCGCAACTTGGGTAAAGTC
139	Z4	306 CTCTCGACCGTCTTGGGGCCCAATGATCCCCGGCGGAGGTCCCGCAACTTGGGTAAAGTC
142	Z5	306 CTCTCGGCCATCTTGGGGCCCAATGATCCCCGGCGGAGaTCGGCGCAATCTGGGTAAAGTC
141	Z1	306 aTCTCGGCCATCTTGGGGCCaAAATGATCCCCGGCGGTAGGTCCCGCAATCTGGGTAAAGTC
139-145	consensus	tTcCaGGCCgTCTTGGGGCCcCAATGATCCCCGGCGGTAGGTCCCGtAAATCTGGGTAAaGTC
145	DK13	
143	Z6	cTCTcGgCCgTCTTGGGGcCcaAAATGATCCCCGGCGgAGgTCCcCGcAAAtTGGGTAAAGTC

FIGURE 6H-3

SEQ ID NO:	ISOLATE	
145	DK13	
143	Z6	367 ATCGATACcCTAAcTTGGGcTTTCGCCGAcCTCATGGGATACATCCCGTcGTAGGCGGCC
144	Z7	367 ATCGATAcTCTAAcTTGGGcTTTCGCCGATcCTCATGGGATACATCCCGTcGTAGGCGGCC
140	Z8	367 ATCGATACCCTAACcTTGGGcTTTCGCCGAcCTCATGGGATACATCCCGTcGTAGGCGGCC
139	Z4	367 ATCGATACCCcTAcGTGGGcTTTCGCCGAcCTCATGGGATACATCCCGTcGTAGGCGGCC
142	Z5	367 ATCGATACCCcTAcGTGGGcTTTCGCCGAcCTCATGGGATACATCCCGTcGTAGGCGGCC
141	Z1	367 ATCGATACCCcTAcGTGGGcTTTCGCCGAcCTCATGGGATACATCCCGTcGTAGGCGGCC
139-145	consensus	ATCGATACcCT-ACgTgCGGcTTcGCCGAcCTCATGGGATACATcCCGcTcGTaGGCGGCC
SEQ ID NO:	ISOLATE	
145	DK13	
143	Z6	428 CCGTGGGtGGcGTGCcAGaGCCcCTGGcGcATGcGcGTcAGGcTcTcTGGAGGACGGGgTCAA
144	Z7	428 CCGTGGGcGGcGTGCcAGGcCCcCTGGcCaATGgTGTAGGGcTgTGGAGGACGGGATCAA
140	Z8	428 CCGTGGGcGGcGTGCcAGGcCCcCTaGCGcATGGcGTAGGGcTcTGGAGGACGGGATtAA
139	Z4	428 CaGTaGgAGGGcGTGCcAGaGCCcCTGGcGcATGGcGTcAGGGcTGTGGAGGACGGGATcAA
142	Z5	428 CcGTgGGgGGcGTGCcAGGcCCcCTGGcGcATGGcGTcAGGGcTGTGGAGGACGGGATtAA
141	Z1	428 CaGTaGGTGGcGTGCcAGGcCCcTGGcGcATGGcGTcAGGGcCCcTGGAGGACGGGATcAA
139-145	consensus	CcGTgGGtGGcGTGCcAGGcCCcTgGCGcATGGcGTcAGGgctgTGGAGGACGGgaTcAA
SEQ ID NO:	ISOLATE	
145	DK13	
143	Z6	489 TTATGCAACAGGGAATcTTCCCGGTGGcTCTCTCTCTATcTTCTCTCTcTGGCACTgCTcTCG
144	Z7	489 TTATGCAACAGGGAATcTTCCCGGTGGcTCTCTCTCTATcTTCTCTCTcTGGCACTTCTTTTCG
140	Z8	489 TTATGCAACAGGGAACcTTCCCGGTGGcTCTCTCTCTATcTTCTCTCTcTGGCACTTCTTTTCG
139	Z4	489 CTATGCAACAGGGAACcTTCTGGTGGcTCTCTCTCTCTATcTTCTCTCTcTGGCACTTCTcTCG
142	Z5	489 CTATGCAACAGGGAATcTTCTGGTGGcTCTCTCTCTCTATcTTCTCTCTcTGGCACTTCTcTCG
141	Z1	489 CTATGCAACAGGGAACcTTCTGGTGGcTCTCTCTCTCTATcTTCTCTCTcTGGCACTTCTcTCG
139-145	consensus	cTATGCAACAGGGAATcTTCCcGGTGGcTCTcTTcTCTATcTCTcTcTgGCACtTcTcTcTCG

NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF
THE ENVELOPE 1...

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Appl. No.: 09/084,691 Atty Docket: NIH240.1CPDV1
REPLACEMENT SHEET

FIGURE 6H-4

<u>SEQ ID NO:</u>	<u>ISOLATE</u>	
145	DK13	550 TGCCTgACTGTtCCCGctTCGGCC
143	Z6	550 TGCCTaACTGTtCCCCaCCTCGGCC
144	Z7	550 TGCCTgACTGTtCCCGCCtCGGCC
140	Z8	550 TGCCTaACcGTcCCAGCGTctGCT
139	Z4	550 TGCCTcACTGTtCCAGCGTCgGCT
142	Z5	550 TGCTTGACAACACCGGCATCcGCT
141	Z1	550 TGCCtGACAACACCaGCATCtGCC
139-145	consensus	TGCcTgACTgttCC-gC-TCgGCC

FIGURE 6I-1

SEQ ID NO:	ISOLATE
153	SA11
152	SA6
146	SA4
147	SA5
148	SA7
149	SA1
150	SA3
151	SA13
146-153	consensus
1 ATGAGCACGAATCCTAAACCTCAAAGAAAAAACCaAAAGAAAAACCAAAACCGCGCCGCCCCACAGG	
1 ATGAGCACGAATCCTAAACCTCAAAGAAAAAACCaAAAGAAAAACCAAAACCGCGCCGCCCCACAGG	
1 ATGAGCACGAATCCTAAACCTCAAAGAAAAAACCaAAAGAAAAACCAAAACCGCGCCGCCCCACAGG	
1 ATGAGCACGAATCCTAAACCTCAAAGAAAAAACCaAAAGAAAAACCAAAACCGCGCCGCCCCACAGG	
1 ATGAGCACGAATCCTAAACCTCAAAGAAAAAACCaAAAGAAAAACCAAAACCGCGCCGCCCCACAGG	
1 ATGAGCACGAATCCTAAACCTCAAAGAAAAAACCaAAAGAAAAACCAAAACCGCGCCGCCCCACAGG	
1 ATGAGCACGAATCCTAAACCTCAAAGAAAAAACCaAAAGAAAAACCAAAACCGCGCCGCCCCACAGG	
1 ATGAGCACGAATCCTAAACCTCAAAGAAAAAACCaAAAGAAAAACCAAAACCGCGCCGCCCCACAGG	
ATGAGCACGAATCCTAAACCTCAAAGAAAAAACCaAAAGAAAAACCAAAACCGCGCCGCCCCACAGG	
62 ACGTCAAGTTCGCCGGCGGTGGTCAGATCGTTGGTGGAGTTTACTTGTTCGCCGCGCAGGGG	
62 ACGTCAAGTTCGCCGGCGGTGGTCAGATCGTTGGTGGAGTTTACTTGTTCGCCGCGCAGGGG	
62 ACGTCAAGTTCGCCGGCGGTGGTCAGATCGTTGGTGGAGTTTACTTGTTCGCCGCGCAGGGG	
62 ACGTCAAGTTCGCCGGCGGTGGTCAGATCGTTGGTGGAGTTTACTTGTTCGCCGCGCAGGGG	
62 ACGTCAAGTTCGCCGGCGGTGGTCAGATCGTTGGTGGAGTTTACTTGTTCGCCGCGCAGGGG	
62 ACGTCAAGTTCGCCGGCGGTGGTCAGATCGTTGGTGGAGTTTACTTGTTCGCCGCGCAGGGG	
62 ACGTCAAGTTCGCCGGCGGTGGTCAGATCGTTGGTGGAGTTTACTTGTTCGCCGCGCAGGGG	
62 ACGTCAAGTTCGCCGGCGGTGGTCAGATCGTTGGTGGAGTTTACTTGTTCGCCGCGCAGGGG	
ACGTCAAGTTCGCCGGCGGTGGTCAGATCGTTGGTGGAGTTTACTTGTTCGCCGCGCAGGGG	
123 CCCTaGgtTGGGTGTGCGCGCGACTCGGAAGAATTTCaGAACGGTCGCAACCCCGTGGgCGG	
123 CCCTcGtaTGGGTGTGCGCGCGACTCGGAAGAATTTCgGAACGGTCGCAACCCCGTGGaCGG	
123 CCCTAGgtTGGGTGTGCGCGCGACTCGGAAGACTTCAGAACGGTCGCAACCCCGTGGGCGG	
123 CCCTAGaTTGGGTGTGCGCGCGACTCGGAAGACTTCAGAACGGTCGCAACCCCGTGGGCGG	
123 CCCTAGGTGGGTGTGCGCGCGACTCGGAAGAATTTCAGAACGGTCGCAACCCCGTGGGCGG	
123 CCCAGGTGGGTGTGCGCGCGACTCGGAAGAATTTCgGAACGGTCGCAACCCCGTGGGCGG	
123 CCCAGGTGGGTGTGCGCGCGACTCGGAAGACTTCAGAACGGTCGCAACCCCGTGGACGG	
123 CCCTaGgtTGGGTGTGCGCGCGaACTCGGAAGACTTCAGAACGGTCGCAACCCCGTGGACGG	
CCCTaGgtTGGGTGTGCGCGCGgACTCGGAAGAATTTCaGAACGGTCGCAACCCCGTGGgCGG	

NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF
THE ENVELOPE 1...

Bukh et al.

Appl. No.: 09/084,691 Atty Docket: NIH240.1CPDV1
REPLACEMENT SHEET

FIGURE 61-2

SEQ ID NO:	ISOLATE	
153	SA11	184 CGTCAGCCTATTCCCAAGCGCGCCAAcCCaCGGGcCGGTCTCTGGGTCAACCCCGGTACC
152	SA6	184 CGTCAGCCTATTCCCAAGCGCGCCAAcCCgCGGtCGGTCTCTGGGTCAACCCCGGTACC
146	SA4	184 CGCCAGCCTATTCCCAAGCGCGCCAAcCCaCGGGCCGGTCTCTGGGTCAACCCCGGTACC
147	SA5	184 CGCCAGCCTATTCCCAAGCGCGCCAAcCCaCGGGCCGGTCTCTGGGTCAACCCCGGTACC
148	SA7	184 CGCCAGCCTATTCCCAAGCGCGCCAAcCCaCGGGCCGGTCTCTGGGTCAACCCCGGTACC
149	SA1	184 CGCCAGCCTATTCCCAAGCGCGCCAAcCCaCGGGCCGGTCTCTGGGTCAACCCCGGTACC
150	SA3	184 CGCCAGCCTATTCCCAAGGtCGCCAGCCaCGGGCCGGTCTCTGGGTCAACCCCGGTACC
151	SA13	184 CGtCAGCCTATcCCCAAGGcGCGCCAGCCaCGGGCCGGTCTCTGGGTCAACCCCGGTACC
146-153	consensus	CGcCAGCCTATtCCCAAGGgCGCCAAcCCaCGGGcCGGTCTCTGGGTCAACCCCGGTACC
SEQ ID NO:	ISOLATE	
153	SA11	245 CTTGGCCCTTTTACGCCAATGAGGGCTCGGGTGGGCAGGGTGGcTGCTCTCCCCCGAGG
152	SA6	245 CTTGGCCCTTTTACGCCAATGAGGGCTCGGGTGGGCAGGGTGGTGTGCTCTCCCCCGAGG
146	SA4	245 CTTGGCCCTTTTACGCCAATGAGGGCTCGGGTGGGCAGGGTGGTGTGCTCTCCCCCGAGG
147	SA5	245 CTTGGCCCTTTTACGCCAATGAGGGCTCGGGTGGGCAGGGTGGTGTGCTCTCCCCCGAGG
148	SA7	245 CTTGGCCCTTTTACGCCAATGAGGGCTCGGGTGGGCAGGGTGGTGTGCTCTCCCCCGAGG
149	SA1	245 CTTGGCCCTTTTACGCCAATGAGGGCTCGGGTGGGCAGGGTGGTGTGCTCTCCCCCGAGG
150	SA3	245 CTTGGCCCTTTTACGCCAATGAGGGCTCGaTGGGCAGGGTGGTGTGCTCTCCCCCGAGG
151	SA13	245 CTTGGCCCTTTATGCCAATGAGGGCTCGgTGGGCAGGGTGGTGTGCTCTCCCCCGAGG
146-153	consensus	CTTGGCCCTTTTAcGCCAATGAGGGCTCGgTGGGCAGGGTGGtTGCTCTCCCCCGAGG
SEQ ID NO:	ISOLATE	
153	SA11	306 CTCTCGGCCTAAcTGGGGCCCCCAATGAccccCGGCGAAGATCGCGCAATTGGGGcAAGGTC
152	SA6	306 CTCTCGGCCTAAcTGGGGCCCCCAATGACccccCGGCGAAGATCGCGCAATTGGGTAAAGTC
146	SA4	306 CTCTCGGCCTAAcTGGGGCCCCCAATGACccccCGGCGAAGATCGCGCAATTGGGTAAAGTC
147	SA5	306 CTCTCGGCCTAAcTGGGGCCCCCAATGACccccCGGCGAAGATCGCGCAATTGGGTAAAGTC
148	SA7	306 CTCTCGGCCTAAcTGGGGCCCCCAATGAccccCGGCGAAGATCGCGCAATTGGGTAAAGTC
149	SA1	306 CTCTCGGCCTAAcTGGGGCCCCCAATGAccccCGGCGAAGATCGCGCAATTGGGTAAAGTC
150	SA3	306 CTCTCGGCCTAgTTGGGGCCCCCAAcGACccccCGGCGAAGATCGCGCAATTGGGTAAAGTC
151	SA13	306 CTCTCGGCCTAaTTGGGGCCCCCAATGACccccCGGCGAAGATCGCGCAATTGGGTAAAGTC
146-153	consensus	CTCTCGGCCTAaTTGGGGCCCCCAATGACccccCGGCGAaAaTCGCGCAATTGGGTAAAGTC

FIGURE 6I-3

SEQ ID NO:	ISOLATE	
153	SA11	367 ATCGATACCCCTAACGTGCGGATTGCGCGACCTCATGGGGTACATCCCGCTCGTAGGGCGGCC
152	SA6	367 ATCGATACCCCTAACGTGCGGATTGCGCGACCTCATGGGGTACATCCCGCTCGTAGGGCGGCC
146	SA4	367 ATCGATACCCCTAACGTGCGGATTGCGCGACCTCATGGGGTACATCCCGCTCGTAGGGCGGCC
147	SA5	367 ATCGATACCCCTAACGTGCGGATTGCGCGACCTCATGGGGTACATCCCGCTCGTAGGGCGGCC
148	SA7	367 ATCGACACCCCTAACaTGCGGATTGCGCGACCTCATGGGGTACATCCCGCTCGTAGGGCGGCC
149	SA1	367 ATCGATACCCCTAACGTGCGGATTGCGCGACCTCATGGGGTACATCCCGCTCGTAGGGCGGCC
150	SA3	367 ATCGATACCCCTAACGTGCGGATTGCGCGACCTCATGGGGTACATCCCGCTCGTAGGGCGGCC
151	SA13	367 ATCGATACCCCTgACGTGCGGATTGCGCGACCTCATGGGGTACATCCCGCTCGTAGGGCGGCC
146-153	consensus	ATCGATACCCCTAACGTGCGGATTGCGCGACCTCATGGGGTACATCCCGCTCGTAGGGCGGCC
SEQ ID NO:	ISOLATE	
153	SA11	428 CCGTTGGGGCGTCGCAAGGGCCCTCGCACACGGTGTGAGAcTCTTGAGGACGGGGTAAA
152	SA6	428 CCGTTGGGGCGTCGCAAGGGCCCTCGCACACGGTGTGAGGGTCTTGAGGACGGGGTAAA
146	SA4	428 CCGTTGGGGCGTCGCAAGGGCCCTCGCACATGGTGTGAGGGTCTTGAGGACGGGGTAAA
147	SA5	428 CCGTTGGGGCGTCGCAAGGGCCCTCGCACATGGTGTGAGGGTCTTGAGGACGGGGTAAA
148	SA7	428 CCGTTGGGGCGTCGCAAGGGCCCTCGCACACGGTGTGAGGGTCTTGAGGACGGGGTAAA
149	SA1	428 CCGTTGGGGCGTCGCAAGGGCCCTCGCACACGGTGTGAGGGTCTTGAGGACGGGGTAAA
150	SA3	428 CCGTTGGGGCGTCGCAAGGGCCCTCGCACAcGGTGTGAGGGTCTTGAGGACGGGGTAAA
151	SA13	428 CCGTTGGGGCGTCGCAAGGGCCCTCGCACAcGGTGTGAGGGTCTTGAGGACGGGGTAAA
146-153	consensus	CCGTTGGGGCGTCGCAAGGGCCCTCGCACAcGGTGTGAGGGTCTTGAGGACGGGGTAAA
SEQ ID NO:	ISOLATE	
153	SA11	489 tTATGCAACAGGGAATcTtCCCGTTGCTCTTTCTCcATCTTTaTCCTTGCACTTCTCTCG
152	SA6	489 CTATGCAACAGGGAATTTGCCCGTTGCTCTTTCTCTATCTTTgTCCCTTGCACTTCTCTCG
146	SA4	489 CTATGCAACGggGAATTTGCCCGTTGCTCTTTCTCTATCTTTATCCTTGCACTTCTCTCG
147	SA5	489 CTATGCAACAGGGAATTTGCCCGTTGCTCTTTCTCTATCTTTATCCTTGCACTTCTCTCG
148	SA7	489 tTACGCAACAGGGAATcTGCCCGTTGCTCTTTCTCTATCTTTaTCCTTGCACTTCTCTCG
149	SA1	489 CTACGCAACAGGGAATTTGCCCGTTGCTCTTTCTCTATCTTTATCCTTGCACTTCTTTCC
150	SA3	489 CTACGCAACAGGGAATTTACCCCGTTGCTCTTTCTCTATCTTTATCCTTGCACTTCTTTCA
151	SA13	489 CTATGCAACAGGGAATTTACCCCGTTGCTCTTTCTCTATCTTTATCCTTGCACTTCTTTCA
146-153	consensus	CTATGCAACaGGGAATtTgCCCGTTGCTCTTTCTCTcTATCTTTaTCCTTGCACTTCTCTCG

FIGURE 6I-4

<u>SEQ ID NO:</u>	<u>ISOLATE</u>
153	SA11
152	SA6
146	SA4
147	SA5
148	SA7
149	SA1
150	SA3
151	SA13
146-153	consensus

550	TGctTgACCGTCCCgGCCaCTGCA
550	TGcCTaACCGTCCCtGCCTCTGCA
550	TGcCTGACCGTCCCgGCCtCTGCA
550	TGctTGACCGTCCCAGCCTCTGCA
550	TGcCTGACCGTCCCAGCCTCcGCA
550	TGtCTGAtCaTCCCGGCCTCTGCA
550	TGcCTGACCGTCCCgGCCtCTGCA
550	TGcCTGACTGTCCCCGaCCTCTGcC
	TGccTgAccgTCCCggCCtCtGCa

FIGURE 6J-1

SEQ ID NO:	Genotype	
103-154	cons.	
1	ATGAGCACgaaTCCTAAACCTCAAAGAAaAaACCaaAcGtAAcCaaCCgcCGCCcAcagG	
103-124	1	ATGAGCACgAaTCCTAAACCTCAAAGAAaAaACCaaAcGtAAcCaaCCgcCGCCcACAGG
125-134	2	ATGAGCACAAaTCCTAAACCTCAAAGAAaAaACCaaAcGtAAcCaaCCgcCGCCcACAGG
135-138	3	ATGAGCACACTTCCTAAACCTCAAAGAAaAaACCaaAcGtAAcCaaCCgcCGCCcACAGG
139-145	4	ATGAGCACgAATCCTAAACCTCAAAGAAaAaACCaaAcGtAAcCaaCCgcCGCCcATGG
146-153	5	ATGAGCACGAATCCTAAACCTCAAAGAAaAaACCaaAcGtAAcCaaCCgcCGCCcACAGG
154	6	ATGAGCACACCTTCCAAaACCCCAAAGAAaAaACCaaAcGtAAcCaaCCgcCGCCcACAGG
SEQ ID NO:	Genotype	
103-154	cons.	
62	AcgTcaAGTTcCCgGGcGGtGGtCAGATCGTtGGtGGAGTtTactTgtTGCCCGCGCAGGGG	
103-124	1	ACGTCAAGTTCCCGGGcGGtGGtCAGATCGTtGGtGGAGTtTactTgtTGCCCGCGCAGGGG
125-134	2	ACGTCAAGTTCCCGGGcGGcGGcCAGATCGTtGGtGGAGTtTactTgtTGCCCGCGCAGGGG
135-138	3	ACGTCAAGTTCCCGGGTGGCGGACAGATCGTtGGtGGAGTtTactTgtTGCCCGCGCAGGGG
139-145	4	ACGTaAGTTCCCGGGtGGtGGcCAGATCGTtGGtGGAGTtTactTgtTGCCCGCGCAGGGG
146-153	5	ACGTCAAGTTCCCGGGCGGTGGTcAGATCGTtGGtGGAGTtTactTgtTGCCCGCGCAGGGG
154	6	ACGTCAAGTTCCCGGGTGGCGGTcAGATCGTtGGtGGAGTtTactTgtTGCCCGCGCAGGGG
SEQ ID NO:	Genotype	
103-154	cons.	
123	CCCcaGgtTGGGTGTGCGCGcGgaCtaGgaAgaCTTCcGAGCGgTCgCAaCCtcGtGGaaGg	
103-124	1	CCCcaGgtTGGGTGTGCGCGcGgaCtAGGAAGACTTCcGAGCGgTCgCAACCTCGtGGaaGg
125-134	2	CCCcAGgtTGGGTGTGCGCGcCGAcAAGGAagaCTTCcGAGCGaTCCcAGCCcgCGTGGgAGg
135-138	3	CCCACGATTGGGTGTGCGCGCGACGCGTAAaACTTCGAAcGGTcaCAGCCTCGCGGACGa
139-145	4	CCCcaGgtTGGGTGTGCGCGcGgaCTcGgaAGACTTCGGAGCGGTcGCAACCTCGtGGcAGg
146-153	5	CCCtaGgtTGGGTGTGCGCGCGACTCGGAAGACTTCaGAACGGTCGCAACCCCGTGGgCGG
154	6	CCCCCGGTGGGTGTGCGCGCGcGACGAGAAAGACTTCcGAGCGGATCCcAGCCcAGAGGCAGG

FIGURE 6J-2

SEQ ID NO:	Genotype		
103-154	cons.		
184		CGaCagCctATcCCcaAGgtCGcCggcccgagGGcaggtcCTGGGctcagCCcGGgtAcc	
103-124	1	CGaCaacCTATCCCCAAGGctCGcCggCCCCGAGGGcAGGgCCTTGGGctCAGCCcGGgtAcc	
125-134	2	CGCCAGCCCCATCCCGAAAGATCGGCGctCCActGGCAAGtCCTGGGAaaCCaGgATATc	
135-138	3	CGACAGCCCTATCCCCAAGGCGGTGGAGCGAAGGCCGgTCCTTGGGTcAGCCcGGGTACC	
139-145	4	CGtCAGCCCTATCCCCAAGGCaCGtCggtccGAGGGcAGgTCCTTGGGctCAGCCcGGGTACC	
146-153	5	CGcCAGCCCTATtCCCCAAGGCGGCCAacCCaCGGgcCGGTCTCTGGGTCAACCCGGGTACC	
154	6	CGCCAACCTATATACCAAGGCGGCCAGCCCCAGGGCAGGCACtTGGGTcAGCCCGGATACC	
SEQ ID NO:	Genotype		
103-154	cons.		
245		CtTGGCCcctTcTATGgcaAtGAGGgcttcGgTGGGCaGgaTGGcTccTgTcCCcCcGcGG	
103-124	1	CtTGGCCcctCTATgCaAtGAGGGccttgGgTGGGCaGGATGGCTCCTGTcACCCCGtGG	
125-134	2	CtTGGCCcctTgTATGGgAAtGAGGGcctCGGcTGGGCaGGtTGGCTCCTGTCCCCCGcGG	
135-138	3	CTTGGCCcctCTATGTGTAAcGAGGGCTGCGGTGGGCaGGgTGGCTCCTGTCCCCCGCGG	
139-145	4	CtTGGCCcctCTtTAcGGcAAtGAGGGcTGcGGGTGGGCaGGgTGGCTCcTGTcCCcCcGG	
146-153	5	CTTGGCCcctTTTAcGCCAAtGAGGGcCTCGgTGGGCaGGGTGGtTGTCTCCCCCcCGAGG	
154	6	CTTGGCCcctCTTTATGGAAACGAGGGCTGTGGGTGGGCaGGTTGGCTCCTGTCCCCCGCGG	
SEQ ID NO:	Genotype		
103-153	cons.		
306		cTctcggCCtagtTGGGGcCccActGAcCCCCCGCGctaggTCgCGcAAttTGGgtAagGTC	
103-124	1	cTctCGGCCTAgTtGGGGCCCCcAcAGACCCCCCGCGtAGGTcGCGtAAttTGGgtAAGGTC	
125-134	2	tTctCgtCCtcttTGGGGCCCCActGAcCCCCCGCATAgATcGCGcAActTGGgtAagGTC	
135-138	3	CTCCCGTCCATCTTGGGGCCCCAAcGACCCCCCGCGgAGGTCCCCCAATTTGGGTAAaGTC	
139-145	4	cTctcGgCCgTCTTGGGGcCcaATGATCCCCCGCGAGgTccCGcAAttTGGGTAAgGTC	
146-153	5	CTCTCGGCCTAatTGGGGCCCCCAAtGACCCCCCGCGAaaTCGCGCAAtTTGGgtAAGGTC	
154	6	CTCCCGGCCACATTTGGGGCCCCCAATGACCCCCCGCGTCGATCCCCGAATTTGGGTAAAGTC	

FIGURE 6J-3

SEQ ID NO:	Genotype	
103-154	cons.	
367	ATCGATACCCtCACgTGcgGctTcGCCGAcCTCATGGGgTACaTcCCgcTCGTcGGcGccc	
367	ATCGATACCCtCaCaTGCGGCTTcGCCGACCTCATGGGTACATtCCGTCGTcGGcGccc	
367	ATCGATACCCtTaACgTGcgGctTtTGCCGACCTCATGGGgTACaTcCCcGTcGTtGGCGccc	
367	ATCGATACCCtTACGTGCGGAtTCGCCGACCTCATGGGTACATcCCCGTCGTcGGCGCTC	
367	ATCGATACcCTgACgTGcGGcTtTGCCGACCTCATGGGTACATcCCGTCGTaGGCGCCC	
367	ATCGATACCCtTaACgTGCGGAtTCGCCGAcCTCATGGGTACATcCCCGTCGTAGCGGGCC	
367	ATCGATACCCtTAACGTGTGGGTTCGCCGATCTCATGGGTACATtCCCCGTCTGTGGCGCGC	
428	CcgTaGGgGGcGtcCGccaggGCCcTgGCGcATGGcGTcaGgggttcTgGAgGACGGggtGAA	
428	CccTaGGgGGcGctTCCACAGGGCCcTGGCGcATGGcGTCCGgGTtctTGGAgGACGGCGTGAA	
428	CggTtGGaGGcGtCGCCAGAGctCTGGCaCATGGtGTgAGgTcCTGGAgGACGGgaTaaa	
428	CcGTAGGaGGCGTCGCAAGAGCCCTCGCGCATGGCGTGAGGCCCCCTTGAAGACGGGATAAA	
428	CcGTgGGtGGCGTCGCCAGGGCCcTgGCGcATGGcGTcAGGgtgTGGAGGACGGgaTCAA	
428	CCGTtGGGGCGTCGCAAGGGctCTcGCACaCGGTGTAGGgttCTTgAGGACGGGGTAAA	
428	CTTtGGCGGGCGTCGCCGCTGCCCTCGCACATGGCGTGAGGGCAATCGAGGACGGGATCAA	
489	cTatGCAACaGGgAAttTgCCcGGTTGctCtTtTcTcTAtcTtTccTccTgGctcTgcTgTcc	
489	cTatGCAACAGGGAAtcTgCCcGGTTGctCtTtTcTcTATcTtTcTcTgGcttTgGcttTgTcc	
489	tTatGCAACaGGgAAttTgCCcGGTTGctCtTtTcTATcTtTcTgctTtGcccttctGTcc	
489	TTTcGCAACAGGGAActTgCCcGGTTGctCtTtTcTATcTtTcTtTcTtCTGTCTct	
489	cTatGCAACAGGGAAtcTtTCCcGGTTGctCtTtTcTATcTtTcTtTgGAcTtctTcTCG	
489	cTatGCAACaGGgAAttTgCCcGGTTGctCtTtTcTcTAtcTtTtTcTtTgGAcTtctTcTCg	
489	TTATGCAACAGGGAATcTCCcGGTTGctCtTtTcTcTATcTtTcTtTtTgGAcTtctTcTCg	
SEQ ID NO:	Genotype	
103-154	cons.	
103-124	1	
125-134	2	
135-138	3	
139-145	4	
146-153	5	
154	6	
SEQ ID NO:	Genotype	
103-154	cons.	
103-124	1	
125-134	2	
135-138	3	
139-145	4	
146-153	5	
154	6	
SEQ ID NO:	Genotype	
103-154	cons.	
103-124	1	
125-134	2	
135-138	3	
139-145	4	
146-153	5	
154	6	

FIGURE 6J-4

<u>SEQ ID NO:</u>	<u>Genotype</u>	
103-154	cons.	
103-124	1	550 TGcctgaccgtccCagcttCtgct
125-134	2	550 TGttTgACcatccCaGctTCcGct
135-138	3	550 TGCatCaCagtgcCaGtgTCtGct
139-145	4	550 TGctTAaTTcATCCaGCAGCTAGT
146-153	5	550 TGccTgACTgttCCagCgTCgGCC
154	6	550 TGccTgAccgTCCCGgCCtCtGCa
		550 TGCCTCACAAAGCCAGCTTCGGCT

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SEQ ID NO:	Genotype
103-108	I/1a
109-124	I/1b
125-128	I/1/2a
129-133	I/2b
134	2c
135-138	(V)/3a
139	4a
141	4b
143	4c
145	4d
146	4f
147-153	5a
154	6a

SEQ ID NO:	Genotype
103-108	I/1a
109-124	I/1b
125-128	I/1/2a
129-133	I/2b
134	2c
135-138	3a
139	3b
141	4b
143	4c
145	4d
146-153	5a
154	6a

SEQ ID NO:	Genotype
103-108	I/1a
109-124	I/1b
125-128	I/1/2a
129-133	I/2b
134	2c
135-138	3a
139	3b
141	4b
143	4c
145	4d
146-153	5a
154	6a

FIGURE 6K-2

SEQ ID NO:	Genotype	350	360	370	380	390	400	410	420	430	440	450	460		
103-108	I/1a	TCGCGCAATTGGGTAAGGTTCATCGATACCC	TACGAGGCTTCGCGGACCTCATGGGGTACAT	CCCGCTCGATGGGAGGCTCCGAGGCGGCTCCGCGCATG											
109-124	II/1b	..G..C..TT....t..Ag.....t..CC..c..G..CG..CT..C.....C.....G..A..a..GG.....C..C..CC..t..C..c..a..C..CT..CAGG..CC..G..G..T..	..G..t..Tt....t..Ag.....t..CC..C..a..CG..CT..C.....C.....G..A..t..GC.....C..C..CC..cc..A..G..c..CT..CAGG..CC..G..G..t..	..G..C..cG....t..Ag.....t..CC..A..G..CG..CT..T.....C.....G..a..C..CG.....B..C..CC..Gc..t..T..c..TC..CAGA..TC..C..G..t..	..A..c..tT....c..88....t..CA..T..g..TG..TT..T.....C.....G..A..C..TG.....t..C..CC..GG..c..A..C..TC..CAGA..TC..G..A..c..	..G..C..CT....t..AG.....t..CC..A..G..CG..TT..T.....C.....G..A..A..CG.....t..C..CT..CG..T..C..C..CT..CAGA..CC..C..C..T..	..C..C..TT....t..Aa.....t..CC..t..G..CG..aT..C.....C.....G..A..C..GC.....G..A..C..CT..CG..A..a..C..TC..AAGA..CC..C..G..T..	..G..C..TC....t..AG.....t..CC..G..G..CG..CT..C.....C.....A..A..C..GA.....G..C..CC..CG..G..G..C..TC..CAGG..TC..G..G..T..	..C..T..TC....t..AA.....t..CC..G..G..TG..CT..C.....C.....A..A..T..GC.....A..C..CC..TG..G..T..C..TC..CAGG..CC..G..G..T..	..C..C..CT....t..AG.....t..TC..A..t..CG..tT..C.....t.....A..A..C..GC.....A..C..CC..CG..G..C..C..TC..CAGG..CC..G..a..T..	..C..C..CT....t..AG.....t..CC..A..I..CG..CT..C.....C.....A..A..C..GG.....A..C..CC..CG..G..T..C..TC..CAGA..CC..G..G..T..	..C..C..TC....t..AG.....t..CC..G..G..TG..CT..C.....C.....A..A..T..GC.....C..C..CC..AG..A..T..C..TC..CAGG..CT..G..G..T..	..G..C..TT....t..AG.....t..CC..C..G..CG..CT..C.....C.....A..A..C..GC.....G..C..CC..AG..A..A..C..TC..CAGA..CC..G..G..T..	..G..C..tT....t..AG.....t..CC..a..g..CG..AT..C.....C.....G..A..C..GC.....A..C..GC..CG..T..G..C..TC..AAGG..TC..C..A..c..	..C..G..TT....t..AG.....t..CC..A..G..TG..GT..C.....t.....G..A..T..CG.....G..C..CG..TT..G..C..C..TC..GGCT..GC..C..A..T..
125-128	III/2a														
129-133	IV/2b														
134	2c														
135-138	(V)/3a														
139	4a														
141	4b														
143	4c														
145	4d														
146-153	5a														
154	6a														

SEQ ID NO:	Genotype	470	480	490	500	510	520	530	540	550	560	570	
103-108	I/1a	GcGTcaggggttcTgAgGACGcgggTgAcTatGCAACagggAAATTgCCGGTtGctcTtTctATtTccTccTgGctTgTcTgTcTgGctgacggtccCagettcttGct											
109-124	II/1b	-C-CC-gGTC-G-A-----CG-G-C-AT-----A-G-G-C-T-T-----T-T-C-T-C-CC-TC-g--CC-GC-C-T--ccTGACTGTG--CGCTI-agCC											
125-128	III/2a	-c-CC-gGTC-G-g-----CG-G-C-AT-----A-G-tt-g-c-----t-t-c-T-C-CC-ct-g--Tt-Gc-g-c--ttTgACcacc--AGctT-CGct											
129-133	IV/2b	-C-GA-agTC-G-G-----GG-T-T-AT-----A-g-Ct-A-t-----T-c-T-T-C-CT-GC-g--Cc-ac-G-C-CATCACCATT--ggTctI-tGCT											
134	2c	-T-TA-gGTCC-G-A-----GA-A-t-AC-----A-G-Tc-G-T-----T-t-T-T-C-CT-aC-T-T-C-TC-G-g--CtCACAgtG--agTGT-TGCg											
135-138	(V)/3a	-G-GA-gGTTC-G-G-----GA-A-T-AT-----G-G-TT-G-C-----T-T-C-T-C-TC-CT-G--CC-CT-G-T--CATCTCTGTG--AGTTT-CGCC											
139	4a	-C-GA-gGCCCT-A-A-----GA-A-T-Tc-----A-G-CT-G-C-----T-C-T-T-C-CC-TC-T--tc-GT-C-t--CtTAaTTCAI--aGCAG-TAGT											
141	4b	-C-CA-gGCTG-G-G-----GA-T-C-AT-----A-G-Tc-T-C-----T-T-C-T-C-CC-TT-G--AC-Tc-T-G--CCTCACTGTI--AGCGT-GGCT											
143	4c	-C-CA-gGCCG-G-G-----AA-T-C-AC-----A-G-CC-T-T-----T-T-C-T-C-TC-TC-T--AC-Tc-C-G--CCTGACAACA--AGCAT-TGCC											
145	4d	-t-TA-gGCTG-G-G-----GA-C-T-AT-----A-G-tc-T-C-----T-T-c-T-C-CC-CT-G--AC-Tc-T-G--CCTaACTGTI--CaCTT-GGCC											
146-153	4e	-C-CA-gGCTC-G-G-----GG-C-T-AT-----A-G-Tc-T-C-----T-T-C-T-C-CC-CT-G--AC-GC-C-G--CCTGACTGTI--CGCTT-GGCC											
147	4f	-C-CA-gGCCG-G-G-----AA-C-C-AT-----A-G-Tc-T-T-----T-C-T-T-C-CC-AC-T--AC-TT-C-G--CTTGACAACA--GGCAT-CGCT											
148-154	5a	-C-CA-gGCTG-G-G-----GA-C-C-AT-----A-G-CC-T-T-----T-T-C-T-C-CC-CT-G--AC-Tc-C-G--CCTAACCGTC--AGGCT-TGCT											
149	5b	-T-GA-gGtTC-T-G-----GG-A-c-AT-----a-G-Tt-g-C-----T-T-C-t-t-C-Ta-CC-T--AC-Tc-c-g--ccTgaccgTC--ggCct-tGca											
150	5c	-C-GA-gGCCAA-C-G-----GA-C-T-AT-----A-G-Tc-C-C-----T-T-C-T-C-CC-TT-G--AC-AC-C-G--CCTCAACAAG--AGCTT-GGCT											

FIGURE 7A-1

SEQ ID NO:	ISOLATE	
156	US11	1 MSTNPKPQRTKRNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
157	S14	1 MSTNPKPQRTKRNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
158	SW1	1 MSTNPKPQRTKRNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
159	S18	1 MSTNPKPQRTKRNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
160	DR4	1 MSTNPKPQRTKRNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
155	DK7	1 MSTNPKPQRTKRNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
155-160	consensus	MSTNPKPQRTKRNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
SEQ ID NO:	ISOLATE	
156	US11	62 RQIPKARRPEGRTWAQPGYPWPPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
157	S14	62 RQIPKARRPEGRTWAQPGYPWPPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
158	SW1	62 RQIPKARRPEGRTWAQPGYPWPPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
159	S18	62 RQIPKARRPEGRTWAQPGYPWPPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
160	DR4	62 RQIPKARRPEGRTWAQPGYPWPPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
155	DK7	62 RQIPKARRPEGRTWAQPGYPWPPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
155-160	consensus	RQIPKARRPEGRTWAQPGYPWPPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
SEQ ID NO:	ISOLATE	
156	US11	123 IDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEEDGVNYATGNLPGCSFSIFLLALLS
157	S14	123 IDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEEDGVNYATGNLPGCSFSIFLLALLS
158	SW1	123 IDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEEDGVNYATGNLPGCSFSIFLLALLS
159	S18	123 IDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEEDGVNYATGNLPGCSFSIFLLALLS
160	DR4	123 IDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEEDGVNYATGNLPGCSFSIFLLALLS
155	DK7	123 IDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEEDGVNYATGNLPGCSFSIFLLALLS
155-160	consensus	IDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVRVLEEDGVNYATGNLPGCSFSIFLLALLS

NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF
THE ENVELOPE 1...

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FIGURE 7A-2

SEQ ID NO:	ISOLATE	
156	US11	184 CLTVPASA
157	S14	184 CLTVPASA
158	SW1	184 CLTVPASA
159	S18	184 CLTVPASA
160	DR4	184 CLTVPASA
155	DK7	184 CLTVPASA
155-160	consensus	CLTVPASA

SEQ ID NO.	ISOLATE
175	P8
176	IND8
177	S45
178	S9
179	D1
180	P10
181	IND3
182	US6
183	DK1
184	T10
185	SW2
186	SA10
187	HK4
188	HK3
189	T3
190	HK5
191	consensus
192-196	
197	consensus
198-202	
203	consensus
204-208	
209	consensus
210-214	
215	consensus
216-220	
221	consensus
222-226	
227	consensus
228-232	
233	consensus
234-238	
239	consensus
240-244	
245	consensus
246-250	
251	consensus
252-256	
257	consensus
258-262	
263	consensus
264-268	
269	consensus
270-274	
275	consensus
276-280	
281	consensus
282-286	
287	consensus
288-292	
293	consensus
294-298	
299	consensus
300-304	
305	consensus
306-310	
311	consensus
312-316	
317	consensus
318-322	
323	consensus
324-328	
329	consensus
330-334	
335	consensus
336-340	
341	consensus
342-346	
347	consensus
348-352	
353	consensus
354-358	
359	consensus
360-364	
365	consensus
366-370	
371	consensus
372-376	
377	consensus
378-382	
383	consensus
384-388	
389	consensus
390-394	
395	consensus
396-400	
401	consensus
402-406	
407	consensus
408-412	
413	consensus
414-418	
419	consensus
420-424	
425	consensus
426-430	
431	consensus
432-436	
437	consensus
438-442	
443	consensus
444-448	
449	consensus
450-454	
455	consensus
456-460	
461	consensus
462-466	
467	consensus
468-472	
473	consensus
474-478	
479	consensus
480-484	
485	consensus
486-490	
491	consensus
492-496	
497	consensus
498-502	
503	consensus
504-508	
509	consensus
510-514	
515	consensus
516-520	
521	consensus
522-526	
527	consensus
528-532	
533	consensus
534-538	
539	consensus
540-544	
545	consensus
546-550	
551	consensus
552-556	
557	consensus
558-562	
563	consensus
564-568	
569	consensus
570-574	
575	consensus
576-580	
581	consensus
582-586	
587	consensus
588-592	
593	consensus
594-598	
599	consensus
600-604	
605	consensus
606-610	
611	consensus
612-616	
617	consensus
618-622	
623	consensus
624-628	
629	consensus
630-634	
635	consensus
636-640	
641	consensus
642-646	
647	consensus
648-652	
653	consensus
654-658	
659	consensus
660-664	
665	consensus
666-670	
671	consensus
672-676	
677	consensus
678-682	
683	consensus
684-688	
689	consensus
690-694	
695	consensus
696-700	
701	consensus
702-706	
707	consensus
7	

FIGURE 7B-2

SEQ ID NO:	ISOLATE	
175	P8	123 IDTLTCGFADLMGYIPLVGgPLGGvARALAHGVRVvEDGVNYATGNLPGCSFSIFLLALLS
170	IND8	123 IDTLTCGFADLMGYIPLVGAPLGGaARALAHGVRVLEdGVNYATGNLPGCSFSIFLLALLS
162	S45	123 IDTLTCGFADLMGYIPLVGAPLGGaARALAHGVRVLEdGVNYATGNLPGCSFSIFLLALLS
171	S9	123 IDTLTCGFADLMGYIPLVGAPLGGaARALAHGVRVLEdGVNYATGNLPGCSFSIFLLALLS
163	D1	123 IDTLTCGFADLMGYIPLVGAPLGGaARALAHGVRVLEdGVNYATGNLPGCSFSIFLLALLS
165	P10	123 IDTLTCGFADLMGYIPLVGAPLGGaARALAHGVRVLEdGVNYATGNLPGCSFSIFLLALLS
169	IND3	123 IDTLTCGFADLMGYIPLVGAPLGGaARALAHGVRVLEdGVNYATGNLPGCSFSIFLLALLS
164	US6	123 IDTLTCGFADLMGYIPLVGAPLGGaARALAHGVRVLEdGVNYATGNLPGCSFSIFLLALLS
166	DK1	123 IDTLTCGFADLMGYIPLVGAPLGGaARALAHGVRVLEdGVNYATGNLPGCSFSIFLLALLS
167	T10	123 IDTLTCGFADLMGYIPLVGAPLGGaARALAHGVRVLEdGVNYATGNLPGCSFSIFLLALLS
168	SW2	123 IDTLTCGFADLMGYIPLVGAPLGGaARALAHGVRVLEdGVNYATGNLPGCSFSIFLLALLS
161	SA10	123 IDTLTCGFADLMGYIPLVGAPLGGaARALAHGVRVLEdGVNYATGNLPGCSFSIFLLALLS
174	HK4	123 IDTLTCGFADLMGYIPLVGAPLGGaARALAHGVRVLEdGVNYATGNLPGCSFSIFLLALLS
172	HK3	123 IDTLTCGFADLMGYIPLVGAPLGGaARALAHGVRVLEdGVNYATGNLPGCSFSIFLLALLS
176	T3	123 IDTLTCGFADLMGYIPLVGAPLGGaARALAHGVRVLEdGVNYATGNLPGCSFSIFLLALLS
173	HK5	123 IDTLTCGFADLMGYIPLVGAPLGGaARALAHGVRVLEdGVNYATGNLPGCSFSIFLLALLS
161-176	consensus	IDTLTCGFADLMGYIPLVGaPLGGaARALAHGVRVLEdGVNYATGNLPGCsFSIFLLALLS
SEQ ID NO:	ISOLATE	
175	P8	184 CLTiPASA
170	IND8	184 CLTiVPASA
162	S45	184 CLTiPASA
171	S9	184 CLTiPASA
163	D1	184 CLTiPASA
165	P10	184 CLTiPASA
169	IND3	184 CLTiPASA
164	US6	184 CLTiPASA
166	DK1	184 CLTiPASA
167	T10	184 CLTiPASA
168	SW2	184 CLTiPASA
161	SA10	184 CLTiPASA
174	HK4	184 CLTiPASA
172	HK3	184 CLTiPASA
176	T3	184 CLTiPASA
173	HK5	184 CLTiPvSA
161-176	consensus	CLTiPaSA

SEQ ID NO.	ISOLATE
173	HK5
176	T3
172	HK3
174	HK4
161	SA10
168	SW2
167	T10
166	DK1
164	US6
169	IND3
165	P10
163	D1
156	US11
157	S14
158	SW1
159	S18
160	DR4
155	DK7
170	IND8
162	S45
171	S9
175	P8
155-176	consensus

FIGURE 7C-2

SEQ ID NO:	ISOLATE	
173	HK5	62 RQIPKARRPEGRtWAQPGYPWPPLYGnEGMGWAGWLLSPhGSRPsWGPTDPRRRSRNLGKV
176	T3	62 RQIPKARRPEGRaWAQPGYPWPPLYGdEGMGWAGWLLSPRGSRPNWGPTDPRRRSRNLGKV
172	HK3	62 RQIPKARQPEGRtWAQPGYPWPPLYGnEGMGWAGWLLSPRGSRPNWGPTDPRRRSRNLGKV
174	HK4	62 RQIPKARQPEGRtWAQPGYPWPPLYGnEGMGWAGWLLSPRGSRPNWGPTDPRRRSRNLGKV
161	SA10	62 RQIPKARQPEGRtWAQPGYPWPPLYGnEGMGWAGWLLSPRGSRPNWGPTDPRRRSRNLGKV
168	SW2	62 RQIPKARQPEGRtWAQPGYPWPPLYGnEGMGWAGWLLSPRGSRPNWGPTDPRRRSRNLGKV
167	T10	62 RQIPKARQPEGRaWAQPGYPWPPLYGnEGMGWAGWLLSPRGSRPNWGPTDPRRRSRNLGKV
166	DK1	62 RQIPKARRPEGRaWAQPGYPWPPLYGnEGMGWAGWLLSPRGSRPNWGPTDPRRRSRNLGKV
164	US6	62 RQIPKARRPEGRaWAQPGYPWPPLYGnEGMGWAGWLLSPRGSRPNWGPTDPRRRSRNLGKV
169	IND3	62 RQIPKARRPEGRaWAQPGYPWPPLYGnEGMGWAGWLLSPRGSRPNWGPTDPRRRSRNLGKV
165	P10	62 RQIPKARRPEGRaWAQPGYPWPPLYGnEGMGWAGWLLSPRGSRPNWGPTDPRRRSRNLGKV
163	D1	62 RQIPKARRPEGRaWAQPGYPWPPLYGnEGMGWAGWLLSPRGSRPNWGPTDPRRRSRNLGKV
156	US11	62 RQIPKARRPEGRtWAQPGYPWPPLYGnEGMGWAGWLLSPRGSRPNWGPTDPRRRSRNLGKV
157	S14	62 RQIPKARRPEGRtWAQPGYPWPPLYGnEGMGWAGWLLSPRGSRPNWGPTDPRRRSRNLGKV
158	SW1	62 RQIPKARRPEGRtWAQPGYPWPPLYGnEGMGWAGWLLSPRGSRPNWGPTDPRRRSRNLGKV
159	S18	62 RQIPKARRPEGRtWAQPGYPWPPLYGnEGMGWAGWLLSPRGSRPNWGPTDPRRRSRNLGKV
160	DR4	62 RQIPKARRPEGRtWAQPGYPWPPLYGnEGMGWAGWLLSPRGSRPNWGPTDPRRRSRNLGKV
155	DK7	62 RQIPKARRPEGRtWAQPGYPWPPLYGnEGMGWAGWLLSPRGSRPNWGPTDPRRRSRNLGKV
170	IND8	62 RQIPKARRPEGRaWAQPGHPWPPLYGnEGMGWAGWLLSPRGSRPNWGPTDPRRRSRNLGKV
162	S45	62 RQIPKARRPEGRaWAQPGHPWPPLYGnEGMGWAGWLLSPRGSRPNWGPTDPRRRSRNLGKV
171	S9	62 RQIPKARhPEGRaWAQPGYPWPPLYGnEGMGWAGWLLSPRGSRPNWGPTDPRRRSRNLGKV
175	P8	62 RQIPKARrPEGRaWAQPGhWPPLYaNEGLGWAGWLLSPRGSRPNWGPTDPRRRSRNLGKV
155-176	consensus	RQIPKARrPEGRaWAQPGYPWPPLYGnEG-GWAGWLLSPRGSRPsWGPTDPRRRSRNLGKV

FIGURE 7C-3

SEQ ID NO:	ISOLATE	
173	HK5	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEEDGVNYATGNIPGCSFSIFLLALLS
176	T3	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEEDGVNYATGNIPGCSFSIFLLALLS
172	HK3	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEEDGVNYATGNIPGCSFSIFLLALLS
174	HK4	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEEDGVNYATGNIPGCSFSIFLLALLS
161	SA10	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEEDGVNYATGNIPGCSFSIFLLALLS
168	SW2	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEEDGVNYATGNIPGCSFSIFLLALLS
167	T10	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEEDGVNYATGNIPGCSFSIFLLALLS
166	DK1	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEEDGVNYATGNIPGCSFSIFLLALLS
164	US6	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEEDGVNYATGNIPGCSFSIFLLALLS
169	IND3	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEEDGVNYATGNIPGCSFSIFLLALLS
165	P10	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEEDGVNYATGNIPGCSFSIFLLALLS
163	D1	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEEDGVNYATGNIPGCSFSIFLLALLS
156	US11	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEEDGVNYATGNIPGCSFSIFLLALLS
157	S14	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEEDGVNYATGNIPGCSFSIFLLALLS
158	SW1	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEEDGVNYATGNIPGCSFSIFLLALLS
159	S18	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEEDGVNYATGNIPGCSFSIFLLALLS
160	DR4	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEEDGVNYATGNIPGCSFSIFLLALLS
155	DK7	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEEDGVNYATGNIPGCSFSIFLLALLS
170	IND8	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEEDGVNYATGNIPGCSFSIFLLALLS
162	S45	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEEDGVNYATGNIPGCSFSIFLLALLS
171	S9	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEEDGVNYATGNIPGCSFSIFLLALLS
175	P8	123 IDTLTCGFADLMGYIPLVGgPLGGVARALAHGVRVLEEDGVNYATGNIPGCSFSIFLLALLS
155-176	consensus	IDTLTCGFADLMGYIPLVGaPLGGaARALAHGVRVLEEDGVNYATGNIPGCSFSIFLLALLS

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Appl. No.: 09/084,691 Atty Docket: NIH240.1CPDV1
REPLACEMENT SHEET

FIGURE 7C-4

SEQ ID NO:	ISOLATE	
173	HK5	184 CLTtPvSA
176	T3	184 CLTiPaSA
172	HK3	184 CLTtPaSA
174	HK4	184 CLTiPaSA
161	SA10	184 CLTiPaSA
168	SW2	184 CLTiPaSA
167	T10	184 CLTiPaSA
166	DK1	184 CLTiPaSA
164	US6	184 CLTiPaSA
169	IND3	184 CLTiPaSA
165	P10	184 CLTiPaSA
163	D1	184 CLTiPaSA
156	US11	184 CLTVPaSA
157	S14	184 CLTVPaSA
158	SW1	184 CLTVPaSA
159	S18	184 CLTVPaSA
160	DR4	184 CLTVPaSA
155	DK7	184 CLTVPaSA
170	IND8	184 CLTVPaSA
162	S45	184 CLTiPaSA
171	S9	184 CLTiPaSA
175	P8	184 CLTiPaSA
155-176	consensus	CLTiPaSA

FIGURE 7D

SEQ ID NO:	ISOLATE	
179	T9	1 MSTNPKPQRKT:RNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVRTTRKTSERSQPRGR
178	US10	1 MSTNPKPQRKT:RNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
180	T2	1 MSTiPKPQRKT:RNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
177	T4	1 MSTnPKPQRKT:RNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
177-180	consensus	MSTnPKPQRKT:RNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVRaTRKTSERSQPRGR
SEQ ID NO:	ISOLATE	
179	T9	62 RQIPKDRRSTGKSWGKPGYPWPPLYGNEGLGWAGWLLSPRGSRPSWGPpDPRHRSRNVGKV
178	US10	62 RQIPKDRRSTGKSWGKPGYPWPPLYGNEGLGWAGWLLSPRGSRPSWGPtDPRHRSRNVGKV
180	T2	62 RQIPKDRRSTGKSWGKPGYPWPPLYGNEGLGWAGWLLSPRGSRPSWGPNDPRHRSRNVGKV
177	T4	62 RQIPKDRRSTGKSWGKPGYPWPPLYGNEGLGWAGWLLSPRGSRPSWGPNDPRHRSRNVGKV
177-180	consensus	RQIPKDRRSTGKSWGKPGYPWPPLYGNEGLGWAGWLLSPRGSRPSWGPnDPRHRSRNVGKV
SEQ ID NO:	ISOLATE	
179	T9	123 IDTLTCGFADLMGYIPVVGAPLGGVARALAHGVRVLEdGVNYATGNLPGCSFSIFLLALLS
178	US10	123 IDTLTCGFADLMGYIPVVGAPLGGVARALAHGVRVLEdGVNYATGNLPGCSFSIFLLALLS
180	T2	123 IDTLTCGFADLMGYIPVVGAPLGGVARALAHGVRVLEdGVNYATGNLPGCSFSIFLLALLS
177	T4	123 IDTLTCsIADLMGYvPVVGgPLGGVARALAHGVRVLEdGVNYATGNLPGCSFSIFLLALLS
177-180	consensus	IDTLTCgfADLMGYiPVVGaPLGGVARALAHGVRVLEdGVNYATGNLPGCSFSIFLLALLS
SEQ ID NO:	ISOLATE	
179	T9	184 CITtPaSA
178	US10	184 CITiPvSA
180	T2	184 CITiPvSA
177	T4	184 CITiPvSA
177-180	consensus	CITiPvSA

FIGURE 7E

SEQ ID NO:	ISOLATE	
183	DK11	1 MSTNPKPQKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRtTRKTSERSQPRGR
184	SW3	1 MSTNPKPQKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
181	T8	1 MSTNPKPQKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
182	US1	1 MSTNPKPQKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
185	DK8	1 MSTNPKPQKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
181-185	consensus	MSTNPKPQKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRaTRKtSERSQPRGR
SEQ ID NO:	ISOLATE	
183	DK11	62 RQIPKDRRSTGKpWGKPGYPWPPLYGNEGCGWAGWLLSPRGSHPNWGPTDPRHkSRNLGKV
184	SW3	62 RQIPKDRRSTGKsWGKPGYPWPPLYGNEGCGWAGWLLSPRGSHPNWGPTDPRHrSRNLGKV
181	T8	62 RQIPKDRRSTGKsWGKPGYPWPPLYGNEGCGWAGWLLSPRGSRPTWGPTDPRHrSRNLGtV
182	US1	62 RQIPKDRRSTGKsWGKPGYPWPPLYGNEGCGWAGWLLSPRGSRPTWGPTDPRHrSRNLGKV
185	DK8	62 RQIPKDRRSTGKsWGKPGYPWPPLYGNEGCGWAGWLLSPRGSRPTWGPTDPRHrSRNLGKV
181-185	consensus	RQIPKDRRSTGKsWGKPGYPWPPLYGNEGCGWAGWLLSPRGsPtWGPTDPRHrSRNLGKV
SEQ ID NO:	ISOLATE	
183	DK11	123 IDTITCGFADLMGYIPVVGAPVGGVARALAHGVRVLEDGINYATGNLPGCSFSIFLLALLS
184	SW3	123 IDTITCGFADLMGYIPVVGAPVGGVARALAHGVRVLEDGINYATGNLPGCSFSIFLLALLS
181	T8	123 IDTITCGFADLMGYIPVVGAPVGGVARALAHGVRVLEDGINYATGNLPGCSFSIFLLALLS
182	US1	123 IDTITCGFADLMGYIPVVGAPVGGVARALAHGVRVLEDGINYATGNLPGCSFSIFLLALLS
185	DK8	123 IDTITCGFADLMGYIPVVGAPVGGVARALAHGVRVLEDGINYATGNLPGCSFSIFLLALLS
181-185	consensus	IDTITCGFADLMGYIPVVGAPVGGVARALAHGVRVLEDGINYATGNLPGCSFSIFLLALLS
SEQ ID NO:	ISOLATE	
183	DK11	184 CcTVPVSA
184	SW3	184 CFTVPVSA
181	T8	184 CFTVPVSA
182	US1	184 CaTVPVSA
185	DK8	184 CcTVPVSA
181-185	consensus	C-TVPVSA

FIGURE 7F-1

SEQ ID NO:	ISOLATE	
183	DK11	1 MSTNPKPQRTKRNTRRRPQDVKFPGGGQIVGGVYLLPRGPRLGVrTtTRKTSERSQPRGR
184	SW3	1 MSTNPKPQRTKRNTRRRPQDVKFPGGGQIVGGVYLLPRGPRLGVrTtTRKTSERSQPRGR
181	T8	1 MSTNPKPQRTKRNTRRRPQDVKFPGGGQIVGGVYLLPRGPRLGVrTtTRKTSERSQPRGR
182	US1	1 MSTNPKPQRTKRNTRRRPQDVKFPGGGQIVGGVYLLPRGPRLGVrTtTRKTSERSQPRGR
185	DK8	1 MSTNPKPQRTKRNTRRRPQDVKFPGGGQIVGGVYLLPRGPRLGVrTtTRKTSERSQPRGR
186	S83	1 MSTNPKPQRTKRNTRRRPQDVKFPGGGQIVGGVYLLPRGPRLGVrTtTRKTSERSQPRGR
178	US10	1 MSTNPKPQRTKRNTRRRPQDVKFPGGGQIVGGVYLLPRGPRLGVrTtTRKTSERSQPRGR
180	T2	1 MSTNPKPQRTKRNTRRRPQDVKFPGGGQIVGGVYLLPRGPRLGVrTtTRKTSERSQPRGR
179	T9	1 MSTNPKPQRTKRNTRRRPQDVKFPGGGQIVGGVYLLPRGPRLGVrTtTRKTSERSQPRGR
177	T4	1 MSTNPKPQRTKRNTRRRPQDVKFPGGGQIVGGVYLLPRGPRLGVrTtTRKTSERSQPRGR
177-186	consensus	MSTnPKPQRTKRNTRRRPQDVKFPGGGQIVGGVYLLPRGPRLGVrTtTRKTSERSQPRGR
183	DK11	62 RQIPKDRRSTGKpWGKPGYPWPPLYGNEGCGWAGWLLSPRGSHPNWGPTDPRHkSRNLGKV
184	SW3	62 RQIPKDRRSTGKsWGKPGYPWPPLYGNEGCGWAGWLLSPRGSHPNWGPTDPRHRSRNLGKV
181	T8	62 RQIPKDRRSTGKsWGKPGYPWPPLYGNEGCGWAGWLLSPRGSRPTWGPTDPRHRSRNLGrV
182	US1	62 RQIPKDRRSTGKsWGKPGYPWPPLYGNEGCGWAGWLLSPRGSRPTWGPTDPRHRSRNLGKV
185	DK8	62 RQIPKDRRSTGKsWGKPGYPWPPLYGNEGCGWAGWLLSPRGSRPTWGPTDPRHRSRNLGKV
186	S83	62 RQIPKDRRSTGKsWGKPGYPWPPLYGNEGCGWAGWLLSPRGSRPTWGPTDPRHRSRNLGKV
178	US10	62 RQIPKDRRSTGKsWGKPGYPWPPLYGNEGCGWAGWLLSPRGSRPTWGPTDPRHkSRNLGKV
180	T2	62 RQIPKDRRSTGKsWGKPGYPWPPLYGNEGCGWAGWLLSPRGSRPTWGPTDPRHRSRNVGKV
179	T9	62 RQIPKDRRSTGKsWGKPGYPWPPLYGNEGCGWAGWLLSPRGSRPTWGPTDPRHRSRNVGKV
177	T4	62 RQIPKDRRSTGKsWGKPGYPWPPLYGNEGCGWAGWLLSPRGSRPTWGPTDPRHRSRNVGKV
177-186	consensus	RQIPKDRRSTGKsWGKPGYPWPPLYGNEG-GWAGWLLSPRGsrPwWGPTDPRHrSRNlGKV

NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF
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Appl. No.: 09/084,691 Atty Docket: NIH240.1CPDV1
REPLACEMENT SHEET

FIGURE 7F-2

SEQ ID NO:	ISOLATE	
183	DK11	123 IDTITCGFADLMGYIPVVGAPVGGVARALAHGVRVLEGGINNYATGNNLPGCSFSIFLLALLS
184	SW3	123 IDTITCGFADLMGYIPVVGAPVGGVARALAHGVRVLEGGINNYATGNNLPGCSFSIFLLALLS
181	T8	123 IDTITCGFADLMGYIPVVGAPVGGVARALAHGVRVLEGGINNYATGNNLPGCSFSIFLLALLS
182	US1	123 IDTITCGFADLMGYIPVVGAPVGGVARALAHGVRVLEGGINNYATGNNLPGCSFSIFLLALLS
185	DK8	123 IDTITCGFADLMGYIPVVGAPVGGVARALAHGVRVLEGGINNYATGNNLPGCSFSIFLLALLS
186	S83	123 IDTLTCGFADLMGYIPVVGAPVGGVARALAHGVRVLEGGINNYATGNNLPGCSFSIFLLALLS
178	US10	123 IDTLTCGFADLMGYIPVVGAPVGGVARALAHGVRVLEGGINNYATGNNLPGCSFSIFLLALLS
180	T2	123 IDTLTCGFADLMGYIPVVGAPVGGVARALAHGVRVLEGGINNYATGNNLPGCSFSIFLLALLS
179	T9	123 IDTLTCGFADLMGYIPVVGAPVGGVARALAHGVRVLEGGINNYATGNNLPGCSFSIFLLALLS
177	T4	123 IDTLTCSLADLMGYVPVVGgPLGGVARALAHGVRVLEGGINNYATGNNLPGCSFSIFLLALLS
177-186	consensus	IDT-TCGfADLMGYiPVVGaPvGGVARALAHGVRVLEGGiNYATGNNLPGCSFSIFLLALLS
SEQ ID NO:	ISOLATE	
183	DK11	184 CcTVPVSA
184	SW3	184 CFTVPVSA
181	T8	184 CFTVPVSA
182	US1	184 CaTVPVSA
185	DK8	184 CcTVPVSA
186	S83	184 CIsVPVSA
178	US10	184 CITiPVSA
180	T2	184 CITiPVSA
179	T9	184 CITtPaSA
177	T4	184 CITiPVSA
177-186	consensus	CitvPvSA

FIGURE 7G

SEQ ID NO:	ISOLATE	
189	S2	1 MSTLPKPQPKTKRNTIRRPQDVKFPGGGQIVGGVYVLPRRGPRLGVRATRKTSERSQPRGR
187	HK10	1 MSTLPKPQPKTKRNTIRRPQDVKFPGGGQIVGGVYVLPRRGPRLGVRATRKTSERSQPRGR
190	DK12	1 MSTLPKPQPKTKRNTIRRPQDVKFPGGGQIVGGVYVLPRRGPRLGVRATRKTSERSQPRGR
188	S52	1 MSTLPKPQPKTKRNTIRRPQDVKFPGGGQIVGGVYVLPRRGPRLGVRATRKTSERSQPRGR
187-190	consensus	MSTLPKPQPKTKRNTIRRPQDVKFPGGGQIVGGVYVLPRRGPRLGVRATRKTSERSQPRGR
SEQ ID NO:	ISOLATE	
189	S2	62 RQIPKARRSEGRSWAQPGYPWPPLYGNEGCGWAGWLLSPRGSRPSWGPNDPRRRSRNLGKV
187	HK10	62 RQIPKARRSEGRSWAQPGYPWPPLYGNEGCGWAGWLLSPRGSRPSWGPNDPRRRSRNLGKV
190	DK12	62 RQIPKARRSEGRSWAQPGYPWPPLYGNEGCGWAGWLLSPRGSRPSWGPNDPRRRSRNLGKV
188	S52	62 RQIPKARRSEGRSWAQPGYPWPPLYGNEGCGWAGWLLSPRGSRPSWGPNDPRRRSRNLGKV
187-190	consensus	RQIPKARRSEGRSWAQPGYPWPPLYGNEGCGWAGWLLSPRGSRPSWGPNDPRRRSRNLGKV
SEQ ID NO:	ISOLATE	
189	S2	123 IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRALEDGINFATGNLPGCSFSIFLLALFS
187	HK10	123 IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRALEDGINFATGNLPGCSFSIFLLALFS
190	DK12	123 IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRALEDGINFATGNLPGCSFSIFLLALFS
188	S52	123 IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRALEDGINFATGNLPGCSFSIFLLALFS
187-190	consensus	IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRALEDGINFATGNLPGCSFSIFLLALFS
SEQ ID NO:	ISOLATE	
189	S2	184 CLIHPAAS
187	HK10	184 CLIHPAAS
190	DK12	184 CLIHPAAS
188	S52	184 CLVHPAAS
187-190	consensus	CLIHPAAS

FIGURE 7H-1

SEQ ID NO:	ISOLATE	
194	Z5	1 MSTNPKPQRTKRTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRatRKTSESRQPRGR
193	Z1	1 MSTNPKPQRTKRTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRaARKTSESRQPRGR
192	Z8	1 MSTNPKPQRTKRTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSESRQPRGR
195	Z6	1 MSTNPKPQRTKRTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSESRQPRGR
196	Z7	1 MSTNPKPQRTKRTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRtTRKTSESRQPRGR
191	Z4	1 MSTNPKPQRTKRTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSESRQPRGR
197	DK13	1 MSTNPKPQRTKRTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSESRQPRGR
191-197	consensus	MSTNPKPQRTKRTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRatRKTSESRQPRGR
SEQ ID NO:	ISOLATE	
194	Z5	62 RQIPqARRSEGRSWAQPgyPWPPLYGNEGCGWAGWLLSPRGSRPSWGqNDPRRRSRNLGKV
193	Z1	62 RQIPkARRSEGRSWAQPgyPWPPLYGNEGCGWAGWLLSPRGSRPSWGPNDRRRSRNLGKV
192	Z8	62 RQIPkARRSEGRSWAQPgyPWPPLYGNEGCGWAGWLLSPRGSRPSWGPNDRRRSRNLGKV
195	Z6	62 RQIPkARRSEGRSWAQPgyPWPPLYGNEGCGWAGWLLSPRGSRPSWGPNDRRRSRNLGKV
196	Z7	62 RQIPkARRSEGRSWAQPgyPWPPLYGNEGCGWAGWLLSPRGSRPSWGPNDRRRSRNLGKV
191	Z4	62 RQIPkARQeGRSWAQPgyPWPPLYGNEGCGWAGWLLSPRGSRPSWGPNDRRRSRNLGKV
197	DK13	62 RQIPkARQlEGRSWAQPgyPWPPLYGNEGCGWAGWLLSPRGSRPSWGPNDRRRSRNLGKV
191-197	consensus	RQIPkArRseGRSWAQPgyPWPPLYGNEGCGWAGWLLSPRGSRPSWGpNDPRRRSRNLGKV

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FIGURE 7H-2

SEQ ID NO:	ISOLATE	
194	Z5	123 IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRAl EDGINYATGNLPGCSFSIFLLALfs
193	Z1	123 IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRavedGINYATGNLPGCSFSIFLLALLS
192	Z8	123 IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRavedGINYATGNLPGCSFSIFLLALLS
195	Z6	123 IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRavedGINYATGNLPGCSFSIFLLALLS
196	Z7	123 IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRAl EDGINYATGNLPGCSFSIFLLALLS
191	Z4	123 IDTLTCGFADLMGYIPIVGAPVGGVARALAHGVRavedGINYATGNLPGCSFSIFLLALLS
197	DK13	123 IDTLTCGFADLMGYIPvVGAPVGGVARALAHGVRl l EDGvNYATGNLPGCSFSIFLLALLS
191-197	consensus	IDTLTCGFADLMGYIPIVGAPVGGVARALAHGVRavedGiNYATGNLPGCSFSIFLLALLS
SEQ ID NO:	ISOLATE	
194	Z5	184 CLTTPASA
193	Z1	184 CLTTPASA
192	Z8	184 CLTVPASA
195	Z6	184 CLTVPtSA
196	Z7	184 CLTVPASA
191	Z4	184 CLTVPASA
197	DK13	184 CLTVPASA
191-197	consensus	CLTVPaSa

<u>SEQ ID NO.</u>	<u>ISOLATE</u>
205	SA11
202	SA3
198	SA4
199	SA5
200	SA7
203	SA13
201	SA1
204	SA6
198-205	consensus

1	MSTNPKPQRKTKRNTNRRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPGRG
1	MSTNPKPQRKTKRNTNRRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPGRG
1	MSTNPKPQRKTKRNTNRRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPGRG
1	MSTNPKPQRKTKRNTNRRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPGRG
1	MSTNPKPQRKTKRNTNRRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPGRG
1	MSTNPKPQRKTKRNTNRRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPGRG
1	MSTNPKPQRKTKRNTNRRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPGRG
1	MSTNPKPQRKTKRNTNRRRPQDVKFPGGGQIVGGVYLLPRRGPRMGVRATRKTSERSQPGRG
1	MSTNPKPQRKTKRNTNRrRPQDVKFPGGGQIVGGVYLLPRRGPRlGVRATrkTSErsQPrGr
198-205	consensus

<u>SEQ ID NO.</u>	<u>ISOLATE</u>
205	SA11
202	SA3
198	SA4
199	SA5
200	SA7
203	SA13
201	SA1
204	SA6
198-205	consensus

FIGURE 71-2

SEQ ID NO:	ISOLATE	
205	SA11	123 IDTLTCGFADLMGYIPLVGGPVGGVARALAHGVRaLEDGVNYATGNLPGCCSFSIFILALLS
202	SA3	123 IDTLTCGFADLMGYIPLVGGPVGGVARALAHGVRVLEDGVNYATGNLPGCCSFSIFILALLS
198	SA4	123 IDTLTCGFADLMGYIPLVGGPVGGVARALAHGVRVLEDGVNYATGNLPGCCSFSIFILALLS
199	SA5	123 IDTLTCGFADLMGYIPLVGGPVGGVARALAHGVRVLEDGVNYATGNLPGCCSFSIFILALLS
200	SA7	123 IDTLTCGFADLMGYIPLVGGPVGGVARALAHGVRVLEDGVNYATGNLPGCCSFSIFILALLS
203	SA13	123 IDTLTCGFADLMGYIPLVGGPVGGVARALAHGVRVLEDGVNYATGNLPGCCSFSIFILALLS
201	SA1	123 IDTLTCGFADLMGYIPLVGGPVGGVARALAHGVRVLEDGVNYATGNLPGCCSFSIFILALLS
204	SA6	123 IDTLTCGFADLMGYIPLVGGPVGGVARALAHGVRVLEDGVNYATGNLPGCCSFSIFVLLLS
198-205	consensus	IDTLTCGFADLMGYIPLVGGPVGGVARALAHGVRVLEDGVNYATGNLPGCCSFSIFILALLS
SEQ ID NO:	ISOLATE	
205	SA11	184 CLTVPaTa
202	SA3	184 CLTVPaSA
198	SA4	184 CLTVPaSA
199	SA5	184 CLTVPaSA
200	SA7	184 CLTVPaSA
203	SA13	184 CLTVPtSA
201	SA1	184 CLiPaSA
204	SA6	184 CLtvPaSA
198-205	consensus	CLtvPaSA

FIGURE 7J

SEQ ID NO:	Genotype	
155-206	cons.	1 MSTnPKPQRKTKRNTnRRPQDVKFPGGGQIVGGVILLPRRGPRLGVRaTKtSERSQPRGRROPfPKaRtpeGrswaqGpYpWPLYgnEGGcgWAGW
155-176	type 1	MSTnPKPQRKTKRNTnRRPQDVKFPGGGQIVGGVILLPRRGPRLGVRaTKtSERSQPRGRROPfPKaRtpeGrswaqGpYpWPLYgnEG-GWAGW
177-186	type 2	MSTnPKPQRKTKRNTnRRPQDVKFPGGGQIVGGVILLPRRGPRLGVRaTKtSERSQPRGRROPfPKaRtpeGrswaqGpYpWPLYgnEG-GWAGW
187-190	type 3	MSTnPKPQRKTKRNTnRRPQDVKFPGGGQIVGGVILLPRRGPRLGVRaTKtSERSQPRGRROPfPKaRtpeGrswaqGpYpWPLYgnEG-GWAGW
191-197	type 4	MSTnPKPQRKTKRNTnRRPQDVKFPGGGQIVGGVILLPRRGPRLGVRaTKtSERSQPRGRROPfPKaRtpeGrswaqGpYpWPLYgnEG-GWAGW
198-205	type 5	MSTnPKPQRKTKRNTnRRPQDVKFPGGGQIVGGVILLPRRGPRLGVRaTKtSERSQPRGRROPfPKaRtpeGrswaqGpYpWPLYgnEG-GWAGW
206	type 6	MSTnPKPQRKTKRNTnRRPQDVKFPGGGQIVGGVILLPRRGPRLGVRaTKtSERSQPRGRROPfPKaRtpeGrswaqGpYpWPLYgnEG-GWAGW
155-206	cons.	97 LLSPrGSRpSwGpDPRrSRNlGkVIdTlTCGfADLMGYiPlVGaPlGGVaRALAHGVRvLEDGVNVATGNlPGCSFSIFllALLSCLtYPaSa
155-176	type 1	LLSPrGSRpSwGpDPRrSRNlGkVIdTlTCGfADLMGYiPlVGaPlGGVaRALAHGVRvLEDGVNVATGNlPGCSFSIFllALLSCLtYPaSa
177-186	type 2	LLSPrGSRpSwGpDPRrSRNlGkVIdTlTCGfADLMGYiPlVGaPlGGVaRALAHGVRvLEDGVNVATGNlPGCSFSIFllALLSCLtYPaSa
187-190	type 3	LLSPrGSRpSwGpDPRrSRNlGkVIdTlTCGfADLMGYiPlVGaPlGGVaRALAHGVRvLEDGVNVATGNlPGCSFSIFllALLSCLtYPaSa
191-197	type 4	LLSPrGSRpSwGpDPRrSRNlGkVIdTlTCGfADLMGYiPlVGaPlGGVaRALAHGVRvLEDGVNVATGNlPGCSFSIFllALLSCLtYPaSa
198-205	type 5	LLSPrGSRpSwGpDPRrSRNlGkVIdTlTCGfADLMGYiPlVGaPlGGVaRALAHGVRvLEDGVNVATGNlPGCSFSIFllALLSCLtYPaSa
206	type 6	LLSPrGSRpSwGpDPRrSRNlGkVIdTlTCGfADLMGYiPlVGaPlGGVaRALAHGVRvLEDGVNVATGNlPGCSFSIFllALLSCLtYPaSa